

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

protein - protein search, using sw model

on: November 15, 2000, 12:34:49 : Search time 35.73 Seconds
(without alignments)
264.133 Million cell updates/sec

le: US-09-359-026-2

fect score: 1486

ence: 1 MKRSGGGGGSSKSEILG.....FQRPTQSYVVKIFGPKVHKP 276

ring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

ched: 268485 seqs, 34193795 residues

al number of hits satisfying chosen parameters: 268485

imum DB seq length: 0

imum DB seq length: 2000000000

t-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

abase : A.Geneseq_36.*

- 1: /cgn2_2/gcgdata/geneseq/geneseq/AA1980.DAT.*
- 2: /cgn2_2/gcgdata/geneseq/geneseq/AA1981.DAT.*
- 3: /cgn2_2/gcgdata/geneseq/geneseq/AA1982.DAT.*
- 4: /cgn2_2/gcgdata/geneseq/geneseq/AA1983.DAT.*
- 5: /cgn2_2/gcgdata/geneseq/geneseq/AA1984.DAT.*
- 6: /cgn2_2/gcgdata/geneseq/geneseq/AA1985.DAT.*
- 7: /cgn2_2/gcgdata/geneseq/geneseq/AA1986.DAT.*
- 8: /cgn2_2/gcgdata/geneseq/geneseq/AA1987.DAT.*
- 9: /cgn2_2/gcgdata/geneseq/geneseq/AA1988.DAT.*
- 10: /cgn2_2/gcgdata/geneseq/geneseq/AA1989.DAT.*
- 11: /cgn2_2/gcgdata/geneseq/geneseq/AA1990.DAT.*
- 12: /cgn2_2/gcgdata/geneseq/geneseq/AA1991.DAT.*
- 13: /cgn2_2/gcgdata/geneseq/geneseq/AA1992.DAT.*
- 14: /cgn2_2/gcgdata/geneseq/geneseq/AA1993.DAT.*
- 15: /cgn2_2/gcgdata/geneseq/geneseq/AA1994.DAT.*
- 16: /cgn2_2/gcgdata/geneseq/geneseq/AA1995.DAT.*
- 17: /cgn2_2/gcgdata/geneseq/geneseq/AA1996.DAT.*
- 18: /cgn2_2/gcgdata/geneseq/geneseq/AA1997.DAT.*
- 19: /cgn2_2/gcgdata/geneseq/geneseq/AA1998.DAT.*
- 20: /cgn2_2/gcgdata/geneseq/geneseq/AA1999.DAT.*
- 21: /cgn2_2/gcgdata/geneseq/geneseq/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	Match	Length	DB ID	Description
1	1486	100.0	276	21	Y58995 Arabidopsis circad
2	621	41.8	215	21	Y70004 Casein kinase I; b
3	92.5	6.2	457	21	Y82777 Human chordin rela
4	92.5	6.2	457	21	Y53035 Human secreted pro
5	88	5.9	316	20	Y28668 Salmonella enterit
6	87	5.9	559	20	Y66221 EHEC E. coli trans
7	85.5	5.8	784	20	W87760 Soybean lysine ket
8	84	5.7	947	19	W81168 Transcriptional re
9	84	5.7	947	20	W05904265 Seq ID N
10	84	5.7	1115	18	W22478 Buffy antigen bind
11	84	5.7	1115	21	Y77899 P. vivax DABP bind
12	84	5.7	1264	14	R36730 Ubiquitin-specific

13	83.5	5.6	966	18	W19916 Drosophila melanog
14	83.5	5.6	1972	19	W81171 Human BAZ2-beta pr
15	83	5.6	271	18	W31546 Bloom's syndrome B
16	83	5.6	515	18	W31547 Bloom's syndrome B
17	83	5.6	739	18	W31549 Bloom's syndrome B
18	83	5.6	1417	18	W31548 Bloom's syndrome B
19	83	5.6	1417	18	W31550 Bloom's syndrome B
20	83	5.6	1417	18	W31551 Bloom's syndrome B
21	83	5.6	1418	18	W15264 Bloom's syndrome act
22	82.5	5.6	1115	12	R13457 Duffy receptor, p
23	82	5.5	1245	16	R70106 TNF-R-pl. vivax Du
24	81.5	5.5	156	20	Y37418 Amino acid sequenc
25	80.5	5.4	1726	17	W03385 Truncated Plasmodi
26	78.5	5.3	927	8	P70768 Epstein-Barr virus
27	78	5.2	1959	12	R10562 Mutant protease (d
28	78	5.2	1962	12	R10560 Mutant protease (K
29	78	5.2	1962	12	R10561 Mutant protease (N
30	78	5.2	1962	12	R10557 Mutant protease (A
31	78	5.2	1962	12	R10558 Mutant protease (A
32	78	5.2	1962	12	R10559 Mutant protease (A
33	78	5.2	1962	12	R10563 Mutant protease (K
34	78	5.2	1968	12	R10941 Mutant protease (d
35	78	5.2	1974	12	R10940 Mutant protease (d
36	77.5	5.2	320	21	W90781 Human DPD2 protein
37	77.5	5.2	453	21	Y52015 Human DPD2 protein
38	77.5	5.2	469	21	Y51644 Amino acid sequenc
39	77.5	5.2	614	19	W56097 Bankia gouldi endo
40	77	5.2	875	19	W34987 HCV NS2-NS5B non-s
41	77	5.2	2201	18	W01680 Non-A, non-B viral
42	77	5.2	3010	13	R20091 Non-A, non-B viral
43	77	5.2	3010	13	R20111 Non-A, non-B viral
44	77	5.2	3010	20	Y08423 E3L translation fa
45	76.5	5.1	190	19	W03571

ALIGNMENTS

RESULT 1

Y58995

ID Y58995 standard; Protein; 276 AA.

XX

AC Y58995;

XX

DT 23-MAY-2000 (first entry)

XX

DE Arabidopsis circadian rhythm-associated protein CKB3.

XX

KW CKB3; circadian rhythm; flowering time; protein kinase;

XX

transgenic plant.

XX

OS Arabidopsis thaliana.

XX

PN W0200004762-A1.

XX

PD 03-FEB-2000.

XX

PF 21-JUL-1999; 99WO-US16525.

XX

PR 24-JUL-1996; 96US-0094072.

XX

(RSCG) UNIV CALIFORNIA.

XX

PI Tobin E, Sugano S;

XX

DR WPI; 2000-182483/16.

XX

N-PSDB; 258536.

PT New CKB3 gene and protein sequences used to alter circadian rhythms and

XX

flowering in plants

XX

Claim 3; Fig 3; S1pp; English.

06-MAY-1999; 99US-0306111.

(GENY) GENETICS INST INC.

Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Merberg D;
Treacy M, DiBlasio-Smith E, Widom A;

WPI: 2000-205978/18.
N-PSDB: Z33173.

New polynucleotides encoding secreted human proteins, useful for treating e.g. broken bones, craniofacial defects, periodontal disease, osteoporosis, burns, incisions or ulcers

Claim 32: Page 99-100; 105pp; English

The human chordin related protein and polynucleotides encoding them are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions which involve defects in cartilage, bone or connective tissue formation and damage to cartilage, bone or connective tissue, e.g. broken bones, congenital, trauma-induced, or oncologic-resection-induced craniofacial defects, periodontal disease, defects in the periodontal ligament or attachment apparatus, damage to the periodontal ligament or attachment apparatus, osteoporosis, burns, incisions or ulcers. The proteins may also affect neurons, astrocytic, and glial cell survival and therefore be useful in transplantation and treatment of conditions exhibiting a decrease in neuronal survival and repair. The proteins may also be useful for the treatment of conditions related to other types of tissue, such as nerve, epidermis, muscle, and other organs such as liver, brain, lung, cardiac, pancreas, and kidney tissue. The proteins may further be useful for the treatment of relatively undifferentiated cell populations, such as embryonic cells, or stem cells, to enhance growth and/or differentiation of the cells. The proteins may also have other useful properties characteristic of the IGF-beta superfamily of proteins. Such properties include angiogenic, chemotactic, and/or chemoattractant properties, and effects on cells including induction or inhibition of collagen synthesis, fibrosis, differentiation responses, cell proliferative responses, and responses involving cell adhesion, migration, and extracellular matrices. These properties make the proteins potential agents for wound healing, reduction of fibrosis, and reduction of scar tissue formation. Chordin-related proteins may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs. Chordin-related proteins may also be useful in modulating hematopoiesis by inducing the differentiation of erythroid cells, for suppressing the development of gonadal tumors, or for augmenting the activity of BMPs. The proteins may also have value as a dietary supplement, or as a component of cell culture media.

Sequence 457 AA;

Query Match 6.2%; Score 92.5; DB 21; Length 457;
Best Local Similarity 25.0%; Pred. No. 0.25;
Matches 38; Conservative 22; Mismatches 57; Indels 35; Gaps 7;

127 YDVALDLILVDASNSE-----MFTDEQHEMVESAAMEL--YGLIH-VRYILTTKG 174

12 yifslilillegskteqvhse:ymfkdqkyrvqerwhpylepyalvycvnciseng 71

175 MAAMTERYKNCDFGRCPRVCCGSCLPVQSDIPRSSTVKIYCPKCEDISYPRSKFQGN 234

72 nvl-----csrrvcnvhc:spvhip-----hlcpcrcpdsipvnmkvts 112

235 IDGAYFGTTTPH--LFLM--TYGNLKFQKFTQ 262

113 kseeYngtYqhqlfvaegltgn:qpnqctq 144

RESULI 4

Y53035

ID Y53035 standard; Protein: 457 AA.

AC Y53035;

DT 29-FEB-2000 (first entry)

DE Human secreted protein clone dw665_4 protein sequence SEQ ID NO:76.

KW Human; secreted protein; nutritional; cytokine; cell proliferation;
KW differentiation; immune stimulating; vaccine; suppression;
KW haematopoiesis regulation; tissue growth; activin; inhibin;
KW chemotactic; chemokinetic; haemostatic; thrombolytic; receptor;
KW ligand; anti-inflammatory; cadherin; tumour invasion suppressor;
KW tumour inhibition; gene therapy.

OS Homo sapiens.

PN W09957132-AL.

PD 11-NOV-1999.

PF 07-MAY-1999; 99WO-US09970.

PR 07-MAY-1998; 98US-0084564.

PR 02-JUN-1998; 98US-0087645.

PR 22-JUL-1998; 98US-0093712.

PR 31-JUL-1998; 98US-0094935.

PR 10-AUG-1998; 98US-0095880.

PR 11-AUG-1998; 98US-0096068.

PR 06-MAY-1999; 99US-0096068.

XX (GENY) GENETICS INST INC.

XX Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;

PI Merberg D, Treacy M, Agostino MJ, Steininger RJ, Bowman MR;

PI DiBlasio-Smith E, Widom A;

XX WPI: 2000-052937/04.

DR N-PSDB: Z33353.

XX New polynucleotides encoding secreted human proteins, derived from

PT adult placenta, adult retina, fetal brain, fetal

XX Claim 85; Page 430-432; 492pp; English.

XX The present invention describes new human secreted proteins which were isolated from adult placenta, adult retina, foetal brain, foetal kidney, adult blood, adult brain, adult thyroid, adult bladder, adult neural tissue, adult testes, and adult lymph node cDNA libraries. The human secreted proteins, and the polynucleotides encoding them, are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity. The polynucleotides are also stated to be useful for gene therapy. Z33316 to Z33373 encode human secreted proteins, and Y52998 to Y53060 represent human secreted proteins, given in the present invention.

XX Sequence 457 AA;

Query Match 6.2%; Score 92.5; DB 21; Length 457;

Best Local Similarity 25.0%; Pred. No. 0.25;

Matches 38; Conservative 22; Mismatches 57; Indels 35; Gaps 7;

QY 127 YDVALDLILVDASNSE-----MFTDEQHEMVESAAMEL--YGLIH-VRYILTTKG 174

12 yifsliflllggkteqvkhssetymqdkkkyrvgerwpylepvglyvncieseng 71
175 MAAMTEKYKNCDFGRCPRVFCGGCLPVGSCIDPRSTVKYKPKCEDISYPRSKFOGN 234
772 nvl-----esrvrcpnhvchispnhp-----hlceprcdslppvinkvts 112
235 IFCAYFGTTFPH-LFLM--TYGNIKKPKQPTQ 262
113 kseevngtctyqgelfvaeglfqnrqpnqctq 144

ULT 5

668

Y28668 standard; Protein; 316 AA.

Y28668;

26-OCT-1999 (first entry)

Salmonella enteritidis wild type orfa encoded protein.

Wild type orfa; Salmonella chromosome; Salmonella specific loop; orfx;
orfv; orfw; f76; 0468; Salmonella pathogenicity islet; sifa gene;
Salmonella typhimurium; immune response; genetically modified; vaccine;
Salmonella induced filament; attenuated; humoral; local; cellular;
tumour; hormone; allergen; toxin; pathogen.

Salmonella enteritidis.

W09937759-A2.

29-JUL-1999.

22-JAN-1999; 99WO-BE00007.

24-Sep-1998; 98SP-0870202.

22-JAN-1998; 98SP-0870019.

(UYVR-) UNIV VRLJE BRUSSEL.

De Greve H, Gubbels E, Hernalsteens J;

WPI; 1999-479047/40.

N-PSDB; X89748.

Vaccine containing attenuated Salmonella strain, for generating
protective immune response to Salmonella or other antigens

Example 2; Page 60-61; 78pp; English.

The present protein sequence is encoded by the orfa wild type DNA which
lies within a region of the Salmonella chromosome. The orfa is located
at one end of the 3417bp Salmonella specific loop comprising Salmonella
pathogenicity islet and including orfx, orfa, orfv and orfw. The loop is
flanked by sequences that show homology with the E.coli open reading
frames f76 and 0468. The orfa encoded protein was found to have 26.7%
homology with the S.typhimurium sifa gene product involved in the
production of "Salmonella induced filaments" in infected epithelial cells
and is required for the virulence of this bacterium. A live, genetically
modified Salmonella strain comprising a modification in this wild type
sequence becomes avirulent and can be used to identify virulent
Salmonella strains. Modified attenuated strains can be used to prepare
vaccines for inducing an immune response (humoral, local and cellular)
against infections induced by Salmonella strains and/or other pathogens,
tumours, hormones, allergens, toxins, etc.

Sequence 316 AA;

Query Match 5.9%; Score 88; DB 20; Length 316;
Best Local Similarity 23.0%; Prod. No. 0.44;
Matches 57; Conservative 30; Mismatches 101; Indels 60; Gaps 10;

QY 35 KLEKSTSTSTTSRVFSS-----KQKDPFSFTSTKT-----QLPDVESEINSEGSUVSGSE 84
DB 11 ksmf'ssaisqrsflllwerikdfcdqrstadyikelcdvasppdaq----- 62
QY 85 GDOTSWISWFCNL-----RGNDFF-----CEVEDY10D--DFNLGG:SGQVPYY 127
DB 63 ----rldfcalyelsspsrcgnfhfhykdaecqytnfikdgdipicivirghyy 118
QY 128 DYALD---LILDVDASNSEMTDEQHEMVESAEMLYGLIHVRVYLLTKG----- 174
DB 119 ydlmrtvlcvdtqphlkrysditakastyvceelcclfcprllislsqgiffpvdlnk 178
QY 175 ----MAAMTEKYKNCDFGRCPRVFCGGCLPVGSCIDPRSTV---KIYCKCEDISY 226
DB 179 iketliamaekgnldwkqerkaaisrrinlgiaqadvppiddaiknkaakvientnl 238
QY 227 PRSKFOGN 234
DB 239 knaafepn 246

RESULT 6

Y06221

ID Y06221 standard; Protein; 559 AA.

XX AC Y06221;

XX DT 16-AUG-1999 (first entry)

XX DE FHRC E. coli; translocated intimin receptor (Tir).

XX DE Tir; translocated intimin receptor; Hp90; enterohaemorrhagic;

XX KW EHEC; infection; diagnosis; vaccine.

XX OS Escherichia coli.

XX XX

XX Key Location/Qualifiers

XX FT Misc-difference 453

XX FT /note- "encoded by codon of 1 apparent nucleotide,

XX FT causing frameshift in the DNA sequence"

XX XX

XX PN W09924576-A1.

XX PC 20-MAY-1999.

XX PF 10-NOV-1998; 98WO-CA01042.

XX PR 12-NOV-1997; 97US-0065130.

XX PA (UYVR-) UNIV BRITISH COLUMBIA.

XX PI Devinney R, Finlay BB, Kenny B, Stein M;

XX DR WPI; 1999-337712/28.

XX DR N-PSDB; X58859.

XX PT New translocated intimin receptor useful for treating infection by

XX PT enteropathogenic or enterohaemorrhagic Escherichia coli

XX PS Claim 7; Page 55-58; 91pp; English.

XX CC The present sequence represents Tir, a novel translocated intimin

XX CC receptor (formerly termed Hp90) from an enterohaemorrhagic

XX CC Escherichia coli (EHEC) strain. The sequence was deduced from an

XX CC isolated tir polynucleotide (see X58859). Tir proteins are

XX CC secreted by attaching and effacing pathogens such as EHEC and EPEC

XX CC (see Y06220) E. coli. The bacterial pathogens insert their own

XX CC receptors into mammalian cell surfaces, to which the pathogen then

XX CC adheres to trigger additional host signaling events and actin

XX CC nucleation. Diagnosis of disease caused by pathogenic E. coli can

XX CC be performed by use of antibodies that bind to Tir to detect the

XX CC protein or the use of nucleic acid probes for detection of nucleic

acids encoding Tir polypeptide. Isolated Tir nucleic acids, Tir peptides, a recombinant method for producing recombinant Tir, antibodies which bind to Tir, and a kit for the detection of Tir-producing *E. coli* are provided. A method of immunising a host with Tir to induce a protective immune response is also provided. In addition, Tir fusion proteins can be used in attenuated *E. coli* to induce a cell-mediated immune response to other polypeptides, e.g. antigens. A method for screening for compounds which interfere with the binding of bacterial pathogens to their receptors is further provided.

Sequence 559 AA:

Query Match 5.9%; Score 57; DB 20; Length 559;
Best Local Similarity 30.4%; Pred. No. 1.2;
Matches 31; Conservative 19; Mismatches 42; Indels 10; Gaps 4;
6 SGGGGGSSRSEILGGAIDRKRINDALNKK---LEKSSSTTSRVFSSKDKDPFSFTST 52
358 ssgagvglgailggig-vavtaahrkkgpvqgttttttttsartvenkpannt 416
63 KIQ-----HIVSEISESGSDVSGSEGB--DTSWISWPCNER 96
417 padgnvutpysedmesrismastestfdtsldqpqrir 459

RESULT 7

W87760 standard; Protein: 784 AA.
W87760:

29-MAR-1999 (first entry)

Soybean lysine ketoglutarate reductase.

Lysine ketoglutarate reductase; saccharopine dehydrogenase;
transgenic plant; seed; soybean.

Glycine max.

W09842831-A2.

01-OCT-1998.

27-MAR-1998; 98WO-US06051.

27-MAR-1997; 97US-0824627.

(DUPO) DU PONT DE NEMOURS & CO E I.

Epelbaum SU, Falco SC, McDevitt RB;

WPI: 1999-045135/04.

N-PSDB: V99562.

Nucleic acids and chimeric genes for increasing seed lysine content - comprise sequence encoding all or part of lysine ketoglutarate reductase, useful to improve nutritional quality of seeds from transformed plants

Claim 2; Page 186-188; 231pp; English.

This is the amino acid sequence of a soybean near full-length lysine ketoglutarate reductase (LKR) or saccharopine dehydrogenase (SDH). It was deduced from cDNA (see V99562) obtained from developing seed mRNA by PCR and RACE. Isolated nucleic acids comprising sequences encoding all or part of plant LKR enzymes are new. Also claimed are: (1) a chimeric gene comprising the fragment (or a subfragment) operably linked to a seed specific regulator, where the chimeric gene reduces LKR activity in plant seeds transformed with it; (2) plant cells and seeds in which LKR

CC activity is reduced due to a mutation in the gene encoding LKR or
CC translocator with the chimeric gene; (3) a nucleic acid fragment
CC comprising: (i) chimeric gene above, and (ii) a second chimeric gene,
CC in which a nucleic acid fragment encoding dihydrodipicolinic acid
CC synthase (DHPS) substantially insensitive to lysine inhibition is
CC operably linked to a plant chloroplast transit sequence and to a
CC plant seed-specific regulatory sequence; (4) plants comprising in
CC genome (i) and (ii), especially as fragment of (2); and (5) seeds
CC from (3). The chimeric genes can be used to produce plant cells
CC and seeds with reduced LKR activity, especially in Arabidopsis,
CC corn, soybean, rapeseed, wheat and rice (claimed). LKR is
CC important in controlling free lysine accumulation in plant seeds.
CC LKR activity reduction may be achieved by cloning the claimed
CC fragment, preparing a chimeric gene for cosuppression of LKR,
CC expression of antisense RNA for LKR, and transforming plants with
CC the chimeric gene.

XX Sequence 784 AA:

Query Match 5.8%; Score 85.5; DB 20; Length 784;
Best Local Similarity 20.1%; Pred. No. 2.9;
Matches 57; Conservative 42; Mismatches 103; Indels 81; Gaps 14;
QY 14 SRSEILGGAIDRKRINDALNKKLEKSSSTTSRVFSSKDKDPFSFTSTKTQLDPVSEST 73
DB 243 sfseevga-dnraavidqildstaiasptehdr-fsnqssksiklgkveenglekcs 300
QY 74 D-----SEGSDVSGSEGBDTSWISWPCNERNDPCEVDEYI----- 111
DB 301 dprkkaavlllgagrvcgaemlssfgprss-sqwyktlledrecqtdveivgsl 359
QY 112 -----QDEFNICGLSCQVPYYDYALDITLDVDSNSMPTDEQHE 151
DB 360 kdaeqtveqipnvtgqlqdvmdranlckysqv-----dvvi-----slppsch 405
QY 152 MVESAA-EMLYGLIHVRYILTTKGMAAMTEKYKNC-----DFGRCPRVFCG--QSCLP 202
DB 406 lvanacieikkhltvasyv--dssmslnldkakdegiltgengldpgi---ghmmamkm 460
QY 203 VQSDIPRSSTVVKLYCPKCEDISYPRS-----KFGQNIIDGA 238
DB 461 inqahv-rkgkksftscgglpspeaanplaykfswnpaga 502

RESULT 8

W81168

ID W81168 standard; Protein: 947 AA.

XX AC W81168;

XX DT 05-MAR-1999 (first entry)

XX DE Transcriptional regulatory factor RING3.

XX KW Human; transcriptional regulatory factor; RING3; TSB; cancer;
XX testis specific bromodomain; testicular cell proliferation.

XX OS Homo sapiens.

XX PN W09848015-A1.

XX PD 29-OCT-1998.

XX PF 17-APR-1998; 98WO-JP01782.

XX PR 18-APR-1997; 97JP-0116402.

XX PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX PJ Jones MH;

XX DR WPI: 1998-583658/49.

This is a truncated BLM protein encoded by a mutant gene sequence isolated from a German Bloom's Syndrome sufferer designated "112(NaSch)". The substitution of the base A at the position 889 of the wild type H1-5' gene to the base T results in a stop codon at amino acid position 272. This was one of the seven unique mutations which were identified in a study of 10 people with Bloom's Syndrome. Based on the various mutations, diagnostic tests for Bloom's Syndrome have been developed which use standard sequence analysis techniques to detect the presence of 2 mutated BLM genes or the absence of a wild-type BLM gene. Note: The present sequence does not appear in the specification; it has been made by modifying the H1-5' wild type BLM sequence which is provided in Figure 2 (W15264).

Sequence 271 AA:

Query Match 5.6%; Score 83; DB 18; Length 271;
Best Local Similarity 21.7%; Pred. No. 1.2;
Matches 36; Conservative 17; Mismatches 41; Indels 72; Gaps 5;
26 KRINDALNKKLEKSTSTTSRVPSKSKKDPSPFTST----- 62
129 kksrdtaikklefsspsdlsindwdmdtdtsetsksfvtppqshfvrystaqskk 188
63 -----KTGLPVEGVLDSEGSNWSGSDDTSWISWFCNLKGNDFPC-- 104
189 gkrnlfkaqlttrvkvktdpppse--seqid:eedkddsewis-----sdvicid 239
105 -----EVEDYIQDQFNICGLSGQVYYDYALDILDVDASNSE 143
240 dypiaevhinedaqcsd-----skthlederduse 270

rich completed: November 15, 2000, 13:23:47
time: 2938 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

protein - protein search, using sw model

on: November 15, 2000, 12:57:15 ; Search time 36.78 seconds
(without alignments)
485,450 Million cell updates/sec

ie: US-09-359-026-2
fect score: 1486
quence: 1 MYKRSGGGGSGSSKSEIIG.....PQKPIQSVKPKIFGKVKHP 276

oring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

ched: 182106 seqs, 63460219 residues

al number of hits satisfying chosen parameters: 182106

imum DB seq length: 0
imum DB seq length: 200000000
st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

atabase : PIR 65: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Match	Length	DB	ID	Description
1	1486	100.0	276	2	T49220	regulatory subunit
2	1294	87.1	283	2	T01595	casein kinase II
3	1039.5	70.0	287	2	S47967	casein kinase II
4	1018	68.5	282	2	S47968	casein kinase II
5	621	41.8	215	2	A39459	casein kinase II
6	621	41.8	215	2	C38611	casein kinase II
7	621	41.8	215	2	JN0566	casein kinase II
8	621	41.8	215	2	S14724	casein kinase II
9	621	41.8	215	2	S23405	casein kinase II
10	621	41.8	215	3	JC7269	protein kinase (EC
11	615	41.4	209	2	A25828	casein kinase II
12	604	40.6	231	2	F50126	casein kinase II
13	599	40.3	235	2	T24317	hypothetical prote
14	597.5	40.2	234	2	T24320	hypothetical prote
15	588.5	39.6	234	2	A41036	casein kinase II
16	543	35.5	196	2	S14725	casein kinase II
17	534.5	34.6	258	2	A54307	casein kinase II
18	477.5	32.1	254	2	T40359	casein kinase II
19	446	30.3	278	2	A56421	casein kinase II
20	370.5	24.9	172	2	S24397	stellate protein
21	369.5	24.9	172	2	S24398	stellate protein
22	95.5	6.4	1274	2	T02636	PI protein homolog
23	93.5	6.3	937	2	S58335	hypically regulated
24	92.5	6.2	515	2	T40809	glutamyl-tRNA redu
25	89	6.0	438	2	T45602	glucosyltransferas
26	89	6.0	1211	2	T08540	hypothetical prote
27	87	5.9	852	2	S48945	hypothetical prote
28	86.5	5.8	408	2	T25524	hypothetical prote
29	86.5	5.8	438	2	T35789	probable secreted

30	86	5.8	334	2	A37286	DNA-binding protei
31	86	5.8	737	2	S28030	DNA-binding protei
32	85.5	5.8	560	2	D7C157	DNA polymerase III
33	84.5	5.7	462	2	T08199	hypothetical prote
34	84	5.7	1272	2	S60999	ubiquitin-specific
35	83.5	5.6	691	2	JC6509	rod cyclic nucleot
36	83.5	5.6	920	2	I40614	surface array prot
37	83	5.6	406	2	S38170	SRP40 protein - ye
38	83	5.6	1417	2	A57570	Bloom's syndrome r
39	83	5.6	1902	1	B44858	lactocepin (EC 3.4
40	82.5	5.6	919	2	T21049	hypothetical prote
41	82.5	5.6	1070	2	T30848	Duffy receptor - p
42	82.5	5.6	1752	2	T48965	hypothetical prote
43	82	5.5	311	2	T17698	hypothetical prote
44	82	5.5	527	2	C70397	periplasmic cell d
45	82	5.5	532	2	S46831	probable membrane

ALIGNMENTS

RESULT 1

T49220
regulatory subunit of protein kinase CK2 - Arabidopsis thaliana
N:Alternate names: protein F27H5.40
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Jun-2000 *sequence_revision 02-Jun-2000 *text_change 02-Jun-2000
C:Accession: T49220
R:Rieser, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z25018
A:Accession: T49220
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-276 <RIE>
A:Cross-references: EMBL:AL163852; GSPDB:GN00061; ATSP:F27H5.40
A:Experimental source: cultivar Columbia; BAC clone F27H5
C:Genetics:
A:Gene: ATSP:F27H5.40
A:Map position: 3
A:Introns: 69/1; 142/1; 178/3; 234/1

Query Match 100.0%; Score 1486; DB 2; Length 276;

Best Local Similarity 100.0%; Pred No. 5.8e-118; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYKRSGGGGSGSSRSEIIGGAIIDKKINDALNKKLEKSTSTSTTSRVFSSKDKDPFSFT 60

DB 1 MYKRSGGGGSGSSRSEIIGGAIIDKKINDALNKKLEKSTSTSTTSRVFSSKDKDPFSFT 60

QY 61 STKTQLPDVSESTDSGSDVSGSGEGDTSWISFNCNLRGNDFFCEVDYIQDDFNLCGL 120

DB 61 STKTQLPDVSESTDSGSDVSGSGEGDTSWISFNCNLRGNDFFCEVDYIQDDFNLCGL 120

QY 121 SGQVPYDYALDJLJLDVDASNSMFTDEQHEMVESAEMLYGLIHVRYITITKGMAAMTE 180

DB 121 SGQVPYDYALDJLJLDVDASNSMFTDEQHEMVESAEMLYGLIHVRYITITKGMAAMTE 180

QY 181 KYKNCDFGRCPRVCCGQSCIPVCGSDTPHSSIVKLYCPKCEDISYPRSKFQGNIDGAVF 240

DB 181 KYKNCDFGRCPRVCCGQSCIPVCGSDTPHSSIVKLYCPKCEDISYPRSKFQGNIDGAVF 240

QY 241 GTTFPHLFLMTYGNLAKPKPTQSYVPKIFGKVKHP 276

DB 241 GTTFPHLFLMTYGNLAKPKPTQSYVPKIFGKVKHP 276

RESULT 2

T01595
casein kinase II (EC 2.7.1.-) beta chain F16B22.17 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 19-Feb-1999 *sequence_revision 19-Feb-1999 *text_change 11-Jan-2000

QY	61	SIKTQL-----	-----PDVESEITDSEGSVDVSGSRGDDTISLWSFC	95
DB	47	TITANLIGKQSQNNINHRDSRSASLKNNTVSDDESITDSESDVSGSGDGTISLWSFC	106	
QY	96	NLRGNDFCEVEDYIQDDFNLCGLSGQVPYDYALDLILDVDASNSEMTDEQHEMVES	155	
DB	107	NLRGNDFCEVDNDYIQDDFNLCGLSSLVPYFEYALDILDVSSQGEFTEEGNELIES	166	
QY	156	AAEMLYGLIHVRYILTTKGMAAMTEYKKNCDGRCRPFVCCQSGCLPVGQSDIPRSSTVK	215	
DB	167	AAEMLYGLIHARYILTSKLAAMDLYKNYDFGRCPVYCCGQCLPVGQSQDIPRSSTVK	226	
QY	216	IYCPKEDIYSPRSKFGQNTDGA YFGTITPLFLMTYGNLKPQKPTQSYVPKIFGKFKVK	275	
DB	227	IYCPKEDIYSPRSKVOGQIDGA YFGTITPLFLMTYGHCLKPAKATQNYQVRVEGFKLHK	286	
QY	276	P 276		
DB	287	P 287		

RESULT 4
 S47968
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 A:Variety: Columbia
 C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 20-Jun-2000
 R:Collinge, M.A.; Walker, J.C.
 Plant Mol. Biol. 25, 649-658, 1994
 A:Title: Isolation of an Arabidopsis thaliana casein kinase II beta subunit
 A:Reference number: S47967; MUID:94339478
 A:Accession: S47968
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-282 <COL>
 A:Cross-references: EMBL:U033984; NID:g467974; P:D:g467975
 R:Bevan, M.; Hancock, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Berg
 P.; Wedler, H.; Wedler, R.; Weitzensegger, T.; Pohl, T.M.; Te
 avannagat, T.; Hempel, S.; Kotter, P.; Enlian, K.D.; Rieger, M.; Schaeffer,
 Nature 392, 485-488, 1998
 A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.
 Kriekot, A.; Mocres, I.; Jones, J.D.G.; Eneva, T.; Palme, K.; Bones, V.; Re
 Chalkatzis, N.

A: Cross-references: GB:29734.3; NID:q2245073; PID:q2245122
 C: Geneticks:
 A: Gene: CKB2
 A: Map Position: 4C0P9-4C3845
 C: Superfamily: human casein kinase II beta chain
 C: Keywords: phosphotransferase; protein kinase

Query Match	69.5%	Score 1018:	DB 2:	Length 282:
Best Local Similarity	65.5%	Pred. No. 1.7e-78:		
Matches 190:	Conservative 41:	Mismatches 37:	Indels 22:	Gaps

```

QY 1 MYKERSGGGGGSSRSFELGKAIDPKRRND-----ALNKKLEKSKSTSTTTSRV 48
    |||||  |||  |||||  |||||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1 MYRER---GMVGSKSEV---VDRKRINEIHDRPSMSQPVNGKGVKTSTSVLMGKQ 52
    |||||  |||  |||||  |||||  |||  |||  |||  |||  |||  |||  |||

QY 49 FSSKUDKPPFTSKTOLPQVE---SETDSGCVSVSGSGDDTWSIWFNCLRGNDFCEV 106
    |||||  |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 53 QLHPKESRSRGSISKTIWISDAVOLSDTDSSESVSGSGDDGTWSIWFNCLRGNDFCEV 112

QY 107 DEDYIQDDFNLCGLSHGVPPYDYALDILIDVDASNSMFTDEQRMVYESAAEMLYGHIH 166
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 113 DDDYIQDDFNLCGLSHGVPPYDYALDILIDVESHGEMFTDEQNELYESAAEMLYGHIH 178
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
  
```


[illegible]

C:Accession: S20405; S10898
R:Jedlicki, A.; Hinrichs, M.V.; Allende, C.C.; Allende, J.F.
FEBS Lett. 297, 280-284, 1992
A:Title: The cDNAs coding for the alpha- and beta-subunits of Xenopus laevis casein kinase II
A:Reference number: S20404; MUID:9218381
A:Accession: S20405
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-215 <JED>
A:Cross-references: EMBL:X62376; NID:g64629; FID:g64630
C:Superfamily: human casein kinase II beta chain
C:Keywords: autophosphorylation; phosphoprotein; phosphotransferase; serine/threonine

Query Match 41.8%; Score 621; DB 2; Length 215;
Best Local Similarity 55.7%; Pred. No. 3.6e-45;
Matches 107; Conservative 31; Mismatches 54; Indels 0; Gaps 0;

Qy 83 SEGDDTSWISWFCNLGRNDFCEVDEDIYQDDFNLCGLSGQVPYYDYALDLILDVDASNS 142
Db 1 :: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2 SSSEFVSWSWFCNLGRNEFFCEVDEDIYQKFNLTGLNEQVPHYRQALDMILDEPDEE 61
Qy 143 EMFTDQHMEVSAEMLYGLIHRYIILTTCGMAATEKYKNCDFGRCPRVFCCQSCLP 202
Db 62 LEDPNOSDLTEQAEMLYGLIHARYILNRIGIAQMLEKYQQGDFGVCPRVCENQMLP 121
Qy 203 VQSDIPRSSSTVKIYCPKCEDISYPRSKFOGNIDGAYFGTTFPHLFMTYGNLKPKPTQ 262
Db 122 IGLSDIPGEAMVLYCPKCMGVITPKSSRHHTDGAYFGTGPHMIFMWHPHYRKRPN 181
Qy 263 SYVPKIFGFKVH 274
Db 182 QVPRLYGFKIH 193

RESULT 10
JC7269
protein: kinase (EC 2.7.1.37) CK2 beta chain - common carp
C:Species: Cyprinus carpio (common carp)
C>Date: 22-Jun-2000 #sequence_revision 22-Jun-2000 #text_change 22-Jun-2000
C:Accession: JC7269
R:Verla, M.I.; Kausel, G.; Barrera, R.; Leal, S.; Figueroa, J.; Querada, C.
Biochem. Biophys. Res. Commun. 271, 735-740, 2000
A:Title: Seasonal adaptation modulates the expression of the protein kinase CK2 beta
A:Reference number: JC7269
A:Accession: JC7269
A>Status: preliminary
A:Residues: 1-215 <VER>
A:Cross-references: GB:AFI33088

Query Match 41.8%; Score 621; DB 3; Length 215;
Best Local Similarity 55.7%; Pred. No. 3.6e-45;
Matches 107; Conservative 31; Mismatches 54; Indels 0; Gaps 0;

Qy 83 SEGDDTSWISWFCNLGRNDFCEVDEDIYQDDFNLCGLSGQVPYYDYALDLILDVDASNS 142
Db 1 :: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2 SSSEFVSWSWFCNLGRNEFFCEVDEDIYQKFNLTGLNEQVPHYRQALDMILDEPDEE 61
Qy 143 EMFTDQHMEVSAEMLYGLIHRYIILTTCGMAATEKYKNCDFGRCPRVFCCQSCLP 202
Db 62 LEDPNOSDLIEQAEMLYGLIHARYILNRIGIAQMLEKYQQGDFGVCPRVCENQMLP 121
Qy 203 VQSDIPRSSSTVKIYCPKCEDISYPRSKFOGNIDGAYFGTTFPHLFMTYGNLKPKPTQ 262
Db 122 IGLSDIPGEAMVLYCPKCMGVITPKSSRHHTDGAYFGTGPHMIFMWHPHYRKRPN 181
Qy 263 SYVPKIFGFKVH 274
Db 182 QVPRLYGFKIH 193

RESULT 11

56.28

sein kinase II (EC 2.7.1.-) beta chain - bovine
Species: Bos primigenius taurus (cattle)
Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 10-Dec-1999
Accession: A25828
Takio, K.; Kuenzel, E.A.; Walsh, K.A.; Krebs, E.G.
oc. Natl. Acad. Sci. U.S.A. 84, 4851-4855, 1987
Title: Amino acid sequence of the beta subunit of bovine lung casein kinase II.
Reference number: A25828; MUID:87260687
Accession: A25828
Molecule type: protein
Residues: 1-209 <IAK>
Superfamily: human casein kinase II beta chain
Keywords: phosphotransferase; serine/threonine-specific protein kinase

Query Match 41.4%; Score 615; DB 2; Length 209;
Best Local Similarity 56.4%; Pred. No. 1,le-44;
Matches 106; Conservative 30; Mismatches 52; Indels 0; Gaps 0;

87 DTSMWFCN:WGNDFECVDFVDEYDQDFNLGSLGQVYDYALDILIDVDSNEMFT 146

2 FVSW:SWFGURGNFEFFCEVDKDYDQDFNLGSLGQVYDYALDILIDVDSNEMFT 61

147 DEQHEWVESAAEMLYGLIHVRYILITKGAAMTEKYKNCDFGRCPRVFCGQSCLPVQGS 206

62 PQSGLIFQAAEMLYGLIHVRYILITKGAAMTEKYKNCDFGRCPRVFCGQSCLPVQGS 121

207 DIPRSSTVKYKPCEDISYPSKFCQGNIDGAYFGTTFPHLFLMTYGNLKTQKPIQSYVP 266

122 DIPGEMVLYKPCMCVYTPKSRHHHTDGYFGTGFPHLFLMTYGNLKTQKPIQSYVP 181

267 KTFGPKVH 274

182 KUYGPKIH 189

SULT 12

0126

sein kinase II beta chain [imported] - fission yeast (Schizosaccharomyces pombe)

Species: Schizosaccharomyces pombe

Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000

Accession: T50126

McDougal, R.C.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Harris, D.

blatted to the EMBL Data Library, December 1999

Reference number: 225040

Accession: T50126

Status: preliminary; translated from GB/EMBL/DBJ

Molecule type: DNA

Residues: 1-231 <MCD>

Cross-references: EMBL:AL133361; PIDN:CA562429.1; GSPDB:GN00066; SPDB:SPAC1557.03

Experimental source: strain 972h(-); cosmid 31451

Genetics:

Gene: SPDB:SPAC1851.03

Map position: 1

Introns: 8/2; 101/73

Query Match 40.6%; Score 604; DB 2; Length 231;

Best Local Similarity 57.7%; Pred. No. 1,le-43;

Matches 113; Conservative 25; Mismatches 52; Indels 6; Gaps 3;

y 81 SQSEGRDVS-WLSWFCNLRGNDFECVDEYDQDFNLGSLGQVYDYALDILIDVDSN 138

b 6 SFSESDSQVWUWFI:GLKONFEFFCEVDKDYDQDFNLGSLGQVYDYALDILIDVDSN 65

v 139 ASKSEFTDEQHEWVESAAEMLYGLIHVRYILITKGAAMTEKYKNCDFGRCPRVFCQSC 193

b 66 POLPEEVQDE---VFASARHLYGLIHVRYILITKGAAMTEKYKNCDFGRCPRVFCQSC 121

y 199 SCLPVGQSDIPKSTVKYKPCEDISYPSKFCQGNIDGAYFGTTFPHLFLMTYGNLKTQK 258

b 122 PMLPVGLSDIAHTKSVKLYCPKEDVYTPKSRHHHTDGYFGTGFPHLFLMTYGNLKTQK 181

Qy 259 KPTCSYVVK-FGPKVH 274

Db 182 KSQERYIPRIFGPKVH 197

RESULT 13

T24317

hypothetical protein T01G9.6b - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000

C:Accession: T24317

R:Lennard, N.

submitted to the EMBL Data Library, July 1996

A:Reference number: Z19874

A:Accession: T24317

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-235 <WIL>

A:Cross-references: EMBL:Z75713; PIDN:CA00053.1; GSPDB:GN00019; CESP:T01G9.6b

A:Experimental source: clone T01G9

C:Genetics:

A:Gene: CESP:T01G9.6b

A:Map position: 1

A:Introns: 6/3; 59/1; 123/1; 186/2

C:Superfamily: human casein kinase II beta chain

Query Match 40.3%; Score 599; DB 2; Length 235;

Best Local Similarity 53.1%; Pred. No. 2,8e-43;

Matches 102; Conservative 37; Mismatches 53; Indels 0; Gaps 0;

Qy 83 SFSGDTSWLSWFCNLRGNDFECVDEYDQDFNLGSLGQVYDYALDILIDVDSNS 142

Db 2 SSSEVSWITWFCGRGNFEFFCEVDKDYDQDFNLGSLGQVYDYALDILIDVDSNS 61

Qy 143 EMFTDEQHEWVESAAEMLYGLIHVRYILITKGAAMTEKYKNCDFGRCPRVFCQSCQLP 202

Db 62 IEDNATNIDVLEQAAEMLYGLIHVRYILITKGAAMTEKYKNCDFGRCPRVFCQSCQLP 121

Qy 203 VQSDIPRSSTVKYKPCEDISYPSKFCQGNIDGAYFGTTFPHLFLMTYGNLKTQKPTQ 262

Db 122 IGLSDVPGEMVLYKPCMCVYTPKSRHHHTDGYFGTGFPHLFLMTYGNLKTQKPTQ 181

Qy 263 SYVPKIFGPKVH 274

Db 192 QFVPKLYGPKIH 193

RESULT 14

T24320

hypothetical protein T01G9.6a - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000

C:Accession: T24320

R:Lennard, N.

submitted to the EMBL Data Library, July 1996

A:Reference number: Z19874

A:Accession: T24320

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-234 <WIL>

A:Cross-references: EMBL:Z75713; PIDN:CA00056.1; GSPDB:GN00019; CESP:T01G9.6a

A:Experimental source: clone T01G9

C:Genetics:

A:Gene: CESP:T01G9.6a

A:Map position: 1

A:Introns: 6/3; 59/1; 122/1; 185/2

C:Superfamily: human casein kinase II beta chain

Query Match 40.2%; Score 597.5; DB 2; Length 234;

Best Local Similarity 53.8%; Pred. No. 3,8e-43;

```

atches 105; Conservative 36; Mismatches 47; Indels 7; Gaps 2;

83 SEGDDTSMISWFCNLKGNDFECVDEYIQGDFNLGLSGQVPYDYALDLIDV---DA 139
| : |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |
2 SSSSEVSWITWFCNLKGNDFECVDEYIQGDFNLGLSGQVPYDYALDLIDV---DA 139
| : |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |
140 SNSEMTDQHEHVESAAEMVGLIHVRYLTGKMAANTEKYKNDGFCGCPVFCGCGS 199
| : |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |
62 EDNATND---LVEQAAMVGLIHVRYLTGKMAANTEKYKNDGFCGCPVFCGCGS 199
| : |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |
200 CLPVGGSDIPRSSTVKIYQCKEDISYPSKKEVGNIDGAYFGITFPPLFLMTYGNLKPKQ 259
| : |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |
118 MLPGLSDVPGCEAMVKLYCPRCNVDVVPKSSRHQHTDGSYFGIGFPHMLFFVHPDLRPR 177
| : |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |
260 PTQSYVPKIFGFKVH 274
| : |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |
178 PVTQFVPKLYGFKIH 192
| : |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |

JLT 15
035
ein kinase II (EC 2.7.1.1-) beta chain - Caenorhabditis elegans
pecies: Caenorhabditis elegans
ate: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 10-Dec-1999
cession: A41036; B41036
u. E.: Rubin, C.S.
iol. Chem. 266, 19796-19802, 1991.
itle: Casein kinase II from Caenorhabditis elegans. Cloning, characterization, and de
reference number: A41036; MUID:92011787
cession: A41036
olecule type: DNA
esidues: 1-234 <HUA>
ross-references: GB:M73827; NID:q156245; PID:q156246
cession: B41036
olecule type: mRNA
esidues: 1-234 <HUG2>
ross-references: GB:M73827; NID:q156245; PID:q156246
enetics:
ntrons: 32/1; 54/1; 106/2; 169/2; 232/3
uperfamily: human casein kinase II beta chain
eywords: autophosphorylation; phosphoprotein; phosphotransferase; serine/threonine-ser
Query Match 39.6%; Score 588.5; DB 2; Length 234;
est Local Similarity 53.3%; Pred. No. 2.2e-42;
atches 104; Conservative 36; Mismatches 48; Indels 7; Gaps 2;

63 SEGDDTSMISWFCNLKGNDFECVDEYIQGDFNLGLSGQVPYDYALDLIDV---DA 139
| : |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |
2 SSSSEVSWITWFCNLKGNDFECVDEYIQGDFNLGLSGQVPYDYALDLIDV---DA 139
| : |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |
140 SNSEMTDQHEHVESAAEMVGLIHVRYLTGKMAANTEKYKNDGFCGCPVFCGCGS 199
| : |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |
62 EDNATND---LVEQAAMVGLIHVRYLTGKMAANTEKYKNDGFCGCPVFCGCGS 199
| : |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |
200 CLPVGGSDIPRSSTVKIYQCKEDISYPSKKEVGNIDGAYFGITFPPLFLMTYGNLKPKQ 259
| : |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |
118 MLPGLSDVPGCEAMVKLYCPRCNVDVVPKSSRHQHTDGSYFGIGFPHMLFFVHPDLRPR 177
| : |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |
260 PTQSYVPKIFGFKVH 274
| : |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |
178 PVTQFVPKLYGFKIH 192
| : |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |

arch completed: November 15, 2000, 13:25:10
b time: 1675 sec

```


seqCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

protein - protein search, using sw model

on: November 15, 2000, 13:23:50 : Search time 29.75 seconds
(without alignments)
306.700 Million cell updates/sec

ie: US-09-359-026-2
fect score: 1486
quence: 1 MYKERSGGGGSSRSSEILG.....PQKPTQSVVPK:FG:VKHP 276

oring table: BLCSUM62
Gapox 10.0 , Gapox 0.5

arched: 87953 seqs, 31947931 residues

tal number of hits satisfying chosen parameters: 87933

imum DB seq length: 0
imum DB seq length: 200000000

st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

atabase : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1486	100.0	276	1	KC2D_ARATH
2	1294	87.1	283	1	KC2E_HALVO
3	1039.5	70.0	287	1	KC2B_ARATH
4	1018	68.5	282	1	KC2C_ARATH
5	621	41.8	215	1	KC2B_HARE
6	621	41.8	215	1	KC2B_HUMAN
7	621	41.8	215	1	KC2B_XENLA
8	612	41.2	215	1	KC2B_DROME
9	604	40.6	231	1	KC2B_SCHPO
10	592	39.8	221	1	KC2B_SPOFR
11	588.5	39.6	234	1	KC2L_CABEL
12	538	36.2	219	1	KC2C_DROME
13	514.5	34.6	238	1	KC2C_YEAST
14	446	30.0	278	1	KC2B_YEAST
15	445	29.9	294	1	KC2B_CANAL
16	434.5	29.2	219	1	SSL_DROME
17	370.5	24.9	172	1	STR_DROME
18	92.5	6.2	315	1	HEM_GLOIO
19	92.5	6.2	937	1	HYR_CANAL
20	87	5.9	852	1	YBQ3_YEAST
21	84	5.7	1272	1	YBP2_YEAST
22	83.5	5.6	691	1	CNGL_CANFA
23	83	5.6	406	1	SKAL_YEAST
24	83	5.6	1417	1	BUM_HUMAN
25	83	5.6	1902	1	P2P_LACPA
26	82.5	5.6	1070	1	PVER_PLAVS
27	82	5.5	532	1	YHB7_YEAST
28	81	5.5	2411	1	DAB_DROME
29	80.5	5.4	346	1	IMP_YEAST
30	80	5.4	555	1	NASY_PTCAN
31	80	5.4	770	1	KiPA_EFENT
32	80	5.4	1902	1	FLP_LACLC
33	79.5	5.3	320	1	VP10_RGDV

34	79.5	5.3	827	1	CSG_HALVO
35	79.5	5.3	933	1	SLAP_CAMFE
36	78.5	5.3	490	1	TWST_DROME
37	78.5	5.3	558	1	YCX9_ASTLO
38	78.5	5.3	1002	1	YEMA_DROME
39	78	5.2	510	1	DMP1_BOVIN
40	78	5.2	656	1	GPH1_CANAL
41	78	5.2	1902	1	P2P_LACLA
42	78	5.2	1902	1	P3P_LACLC
43	77.5	5.2	469	1	HPD2_HUMAN
44	77.5	5.2	564	1	HOMA_TABUD
45	77.5	5.2	690	1	CNGL_BOVIN

ALIGNMENTS

RESULT	KC2D_ARATH	STANDARD;	PRI: 276 AA.
ID	081275;		
AC	15-JUL-1999 (Rel. 38, Created)		
DT	15-JUL-1999 (Rel. 38, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	CASEIN KINASE II BETA-5 CHAIN (CK II) (EC 2.7.1.37).		
GN	CKB3		
OS	Arabidopsis thaliana (Mouse-ear cress).		
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;		
OC	Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;		
OC	Brassicales; Brassicaceae; Arabidopsis.		
RN	[1]		
RF	SEQUENCE FROM N.A.		
RX	MEDLINE: 98393763.		
RA	Sugano S., Andronis C., Green R.M., Wang Z.Y., Tobin E.M.;		
RI	"Protein kinase CK2 interacts with and phosphorylates the Arabidopsis		
RI	circadian clock-associated 1 protein.";		
KL	Proc. Natl. Acad. Sci. U.S.A. 95:11020-11025(1998).		
CC	-!- FUNCTION: PLAYS A COMPLEX ROLE IN REGULATING THE BASAL CATALYTIC		
CC	ACTIVITY OF THE ALPHA SUBUNIT (BY SIMILARITY).		
CC	-!- SUBUNIT: TETRAMER COMPOSED OF AN ALPHA CHAIN, AN ALPHA', AND		
CC	TWO BETA-TYPE CHAINS.		
CC	-!- PTM: PHOSPHORYLATED BY ALPHA CHAIN (BY SIMILARITY).		
CC	-!- SIMILARITY: BELONGS TO THE CASEIN KINASE 2 BETA CHAIN FAMILY.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	EMBL: AF068318; AAC33896.1; .		
CC	INTERPRO: IPR000704; .		
DR	PFAM: PF01214; CK.II.beta.1.		
DR	PRINTS: PR00472; CASNKNASE11.		
DR	PROSITE: PS0131; CK2_HETA; 1.		
SO	Transferase: Serine/threonine-protein kinase; phosphorylation.		
SO	SEQUENCE 276 AA; 10798 MW; 611PFC1222B2CC55 CRC64;		

Query Match	100.0%	Score 1466;	DB 1: Length 276;
Best local similarity	100.0%	Prod. No. 8.7e-119;	
Matches 276;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1	MYKERSGGGGSSRSSEILGADRKNALNKKLEKSTSTTTTSKVFSSKDKDPFSFT	60
DB	1	MYKERSGGGGSSRSSEILGADRKNALNKKLEKSTSTTTTSKVFSSKDKDPFSFT	60
OY	61	STKTQLPDVSEFTDSEGSVSGEGDTSWISWFCNLGRNDFCEVDEYDIQDFNLGL	120
DB	61	STKTQLPDVSEFTDSEGSVSGEGDTSWISWFCNLGRNDFCEVDEYDIQDFNLGL	120

121 SGQVYVYDALDILVDASNSSEMTDEQHEMVSAEMLYGLIHVRYILITKGAAMTE 180
 122 SGQVYVYDALDILVDASNSSEMTDEQHEMVSAEMLYGLIHVRYILITKGAAMTE 180
 123 SGQVYVYDALDILVDASNSSEMTDEQHEMVSAEMLYGLIHVRYILITKGAAMTE 180
 181 KYKNDGFGRCPRVFCGSGCLPVGQSDIPRSTVTKYCPKCEDISYPRSKFOGNDGAYF 240
 182 KYKNDGFGRCPRVFCGSGCLPVGQSDIPRSTVTKYCPKCEDISYPRSKFOGNDGAYF 240
 241 GTTFPHLMTYGNLAKPKQKTSYVVKIFGFKVH 276
 242 GTTFPHLMTYGNLAKPKQKTSYVVKIFGFKVH 276
 243 GTTFPHLMTYGNLAKPKQKTSYVVKIFGFKVH 276

RESULT 2
 KC2B_ARATH STANDARD: PRT; 283 AA.
 080507: 15-JUL-1999 (Rel. 38, Created)
 15-JUL-1999 (Rel. 38, Last sequence update)
 15-JUL-1999 (Rel. 38, Last annotation update)
 PUTATIVE CASEIN KINASE II BETA-4 CHAIN (CK II) (EC 2.7.1.37).
 F16322.17
 Arabidopsis thaliana (Mouse-ear cress).
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 brassicales; Brassicaceae; Arabidopsis.
 [1]
 SEQUENCE FROM N.A.
 STRAIN=CV. COLUMBIA;
 Rounsley S.D., Kauf S., Liu X., Ketchum K.A., Crosby M.L.,
 Brandon R.C., Sykes S.M., Mason T.M., Kerlavage A.R., Adams M.D.,
 Somerville C.R., Venter J.C.;
 Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 -!- FUNCTION: PLAYS A COMPLEX ROLE IN REGULATING THE BASAL CATALYTIC
 ACTIVITY OF THE ALPHA SUBUNIT (BY SIMILARITY).
 -!- SUBUNIT: TETRAMER COMPOSED OF AN ALPHA CHAIN, AN ALPHA', AND
 TWO BETA-TYPE CHAINS.
 -!- PTM: PHOSPHORYLATED BY ALPHA CHAIN (BY SIMILARITY).
 -!- SIMILARITY: BELONGS TO THE CASEIN KINASE 2 BETA FAMILY.
 This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 EMBL: AC003672; AAC22470.1;
 INTERPRO: IPR00704;
 PFAM: PF01214; CK_II_beta; 1.
 PRINTS: PR00472; CASKNKASEII.
 PROSITE: PS01101; CK2_BETA; 1.
 Transferase: Serine/threonine-protein kinase; Phosphorylation.
 SEQUENCE 283 AA; 31631 MW; DF5912A79F060797 CRC64;

Query Match 87.1%; Score 1294; DB 1; Length 283;
 Best Local Similarity 87.2%; Pred. No. 1,6e-102;
 Matches 246; Conservative 44; Mismatches 12; Indels 10; Gaps 4;
 1 MYKERSGG---GGGGSSRSSEILGATDRKINDALKKLEKSTSTITSRVFSSKDKDPFSFT 57
 1 MYKDRGGGIMGGGSSRSSEILGATDRKINDALKKLEKSTSTITSRVFSSKDKDPFSFT 58
 58 SFTSTI-KTQL-----POVSESTDSEGSVDVSGEGDDTISWISWFCNLRGNDFCEVDEYIQ 112
 59 PSTSTAKSLRSRSPDVSSTDSEGSVDVSGEGDDTISWISWFCNLRGNDFCEVDEYIQ 118
 113 DDFNLGCGSGOVYVYDALDILVDASNSSEMTDEQHEMVSAEMLYGLIHVRYILIT 172
 119 DDFNLGCGSGOVYVYDALDILVDASNSSEMTDEQHEMVSAEMLYGLIHVRYILIT 178

QY 173 KGMAAATEKYKNCDFGRCPRVFCGSGCLPVGQSDIPRSTVTKYCPKCEDISYPRSKFO 232
 DB 179 KGMAAATEKYKNCDFGRCPRVFCGSGCLPVGQSDIPRSTVTKYCPKCEDISYPRSKFO 238
 QY 233 GNTDGAFTSTTFPHLFLMTYGNLAKPKQKTSYVVKIFGFKVH 274
 DB 239 GNTDGAFTSTTFPHLFLMTYGNLAKPKQKTSYVVKIFGFKVH 280
 RESULT 3
 KC2B_ARATH STANDARD: PRT; 287 AA.
 AC P40228;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE CASEIN KINASE II BETA CHAIN (CK II) (EC 2.7.1.37).
 GN CKB1.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC brassicales; Brassicaceae; Arabidopsis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94339478.
 RA Collinge M.A., Walker J.C.;
 RT "Isolation of an Arabidopsis thaliana casein kinase II beta subunit
 by complementation in Saccharomyces cerevisiae";
 RL Plant Mol. Biol. 25:649-656(1994).
 CC -!- FUNCTION: PLAYS A COMPLEX ROLE IN REGULATING THE BASAL CATALYTIC
 ACTIVITY OF THE ALPHA SUBUNIT (BY SIMILARITY).
 CC -!- SUBUNIT: TETRAMER COMPOSED OF AN ALPHA CHAIN, AN ALPHA', ONE
 BETA CHAIN AND ONE BETA' CHAIN.
 CC -!- PTM: PHOSPHORYLATED BY ALPHA CHAIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE CASEIN KINASE 2 BETA CHAIN FAMILY.
 This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 EMBL: L22563; AAA53233.1;
 INTERPRO: IPR00704;
 PFAM: PF01214; CK_II_beta; 1.
 PRINTS: PR00472; CASKNKASEII.
 PROSITE: PS01101; CK2_BETA; 1.
 Transferase: Serine/threonine-protein kinase; Phosphorylation.
 SEQUENCE 287 AA; 32355 MW; 43C811727B0985EE CRC64;

Query Match 70.0%; Score 1039.5; DB 1; Length 287;
 Best Local Similarity 65.1%; Pred. No. 5.7e-81;
 Matches 196; Conservative 33; Mismatches 39; Indels 39; Gaps 4;
 QY 1 MYKERSGGGGGSSRSSEILGATDRKINDALKKLEKSTSTITSRVFSSKDKDPFSFT 60
 DB 1 MYKDRGGGGGSSRSSEILGATDRKINDALKKLEKSTSTITSRVFSSKDKDPFSFT 46
 QY 61 STKTQL-----PDVSESTDSEGSVDVSGEGDDTISWISWFC 95
 DB 47 TTIANI.GKQSNINHRDSRSASLSKNTVSDSDSDTDSBESDVSGSDGSDTISWISWFC 106
 QY 96 NLRGNDFFCEVDEYIQDQFNLCGSGGVYVYDALDILVDASNSSEMTDEQHEMVSA 155
 DB 107 NLRGNEFFCEVDDYIQDQFNLCGSGSLVPYVEYALDILVDVSSQGENFTEEQNELTES 166
 QY 156 AAFMLYGLIHVRYILITTKMAAMTEKYKNCDFGRCPRVFCGSGCLPVGQSDIPRSTVTK 215
 DB 167 AAFMLYGLIHVRYILITTKMAAMTEKYKNCDFGRCPRVFCGSGCLPVGQSDIPRSTVTK 226

122 IGLSDIPGEAMVKLYCPKCMGVYFKSSRHHTDGVFG7SFPEMLFW7PEYRPKR2AN 18:
263 SYVPK1CFKVVH 274
192 QFVRLXGFKIH 19:
SUBIT 6
2B_HUMAN
KCB2B_HUMAN STANDARD; PRT; 215 AA.
P13862; P07312;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CASEIN KINASE II BETA CHAIN (CK II) (EC 2.7.1.37) (PHOSVITIN).
CSNK2B OR CK2N.
Homo sapiens (Human), Mus musculus (Mouse), Rattus norvegicus (Rat),
Bos taurus (Bovine), Sus scrofa (Pig),
Oryctolagus cuniculus (Rabbit), and Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
[1]
SEQUENCE FROM N.A.
SPECIES=HUMAN;
MEDLINE; 89325340.
Jakobi R., Voss R., Pyerin W.;
"Human phosvitin/casein kinase type II. Molecular cloning and
sequencing of full-length cDNA encoding subunit beta.";
Eur. J. Biochem. 183:227-233(1989).
[2]
SEQUENCE FROM N.A.
SPECIES=HUMAN;
MEDLINE; 91310643.
Voss A., Wirner G., Jacobi R., Hewitt N., Schwager C.,
Zimmermann J., Ansorge W., Pyerin W.;
"Structure of the gene encoding human casein kinase II subunit beta.";
J. Biol. Chem. 266:13706-13711(1991).
[3]
SEQUENCE FROM N.A.
SPECIES=HUMAN;
MEDLINE; 90105447.
Heller-Harrison R.A., Meisner H., Czech M.P.;
"Cloning and characterization of a cDNA encoding the beta subunit of
human casein kinase II.";
Biochemistry 28:9053-9058(1989).
[4]
SEQUENCE FROM N.A.
SPECIES=MOUSE; STRAIN=BAJB/C;
MEDLINE; 90301488.
Kopatz I., Naiman T., Pli D., Canaan D.;
"The nucleotide sequence of the mouse cDNA encoding the beta subunit
of casein kinase II.";
Nucleic Acids Res. 18:3639-3649(1990).
[5]
SEQUENCE FROM N.A.
SPECIES=MOUSE; STRAIN=C57BL/6 X CBA; TISSUE=SPLEEN;
MEDLINE; 96079116.
Boidyreff A., Issinger O.G.;
"Structure of the gene encoding the murine protein kinase CK2 beta
subunit.";
Genomics 29:253-256(1995).
[6]
SEQUENCE FROM N.A.
SPECIES=RAT; TISSUE=LIVER;
MEDLINE; 94227842.
Almed K., Davis A., Hanten J., Lambert D., McIvor R.S., Goulet S.A.;
"Cloning of cDNAs encoding the alpha and beta subunits of rat casein
kinase 2 (CK-2): investigation of molecular regulation of CK-2 by
androgens in rat ventral prostate.";
Cell. Mol. Biol. Res. 39:451-462(1993).
[7]
SEQUENCE FROM N.A.

SPECIES=MOUSE, AND PIG;
MEDLINE; 91198153.
Roldyreff A., Plontek K., Schmidt-Spanio J., Issinger O.G.;
"The beta subunit of casein kinase II: Cloning of cDNAs from murine
and porcine origin and expression of the porcine sequence as a fusion
protein.";
Biochim. Biophys. Acta 1068:439-444(1991).
[8]
SEQUENCE OF 4-215.
SPECIES=BOVINE, TISSUE=LUNG;
MEDLINE; 87260687.
Takio K., Kuenzel E.A., Walsh K.A., Krebs E.G.;
"Amino acid sequence of the beta subunit of bovine lung casein kinase
II.";
Proc. Natl. Acad. Sci. U.S.A. 84:4851-4855(1987).
[9]
SEQUENCE FROM N.A.
SPECIES=RABBIT;
MEDLINE; 93185937.
Gupta S.K., Singh J.P.;
"PCR cloning and sequence of two cDNAs encoding the alpha and beta
subunits of rabbit casein kinase-II.";
Gene 124:287-290(1993).
[10]
SEQUENCE FROM N.A.
SPECIES=RABBIT; STRAIN=NEW ZEALAND WHITE;
Gupta S.K., Rothfuss K.J., Singh J.P.;
Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
[11]
SEQUENCE FROM N.A.
SPECIES=CHICKEN;
MEDLINE; 91115855.
Maridor G., Park W., Kreg W., Nigg E.A.;
"Casein kinase II cDNA sequences, developmental expression, and
tissue distribution of mRNAs for alpha, alpha', and beta subunits of
the chicken enzyme.";
J. Biol. Chem. 266:2362-2368(1991).
[12]
FUNCTION: PLAYS A COMPLEX ROLE IN REGULATING THE BASAL CATALYTIC
ACTIVITY OF THE ALPHA SUBUNIT.
[13]
SUBUNIT: TETRAMER COMPOSED OF AN ALPHA CHAIN, AN ALPHA' AND TWO
BETA CHAINS.
[14]
PTM: PHOSPHORYLATED BY ALPHA CHAIN.
[15]
SIMILARITY: BELONGS TO THE CASEIN KINASE 2 BETA CHAIN FAMILY.
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation.
The European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
[16]
EMBL; S56243; AAB35555.1;
EMBL; X16937; CAA34811.1;
EMBL; X16312; CAA34379.1;
EMBL; X57152; CAA40442.1;
EMBL; X80685; CAA56700.1;
EMBL; M30448; AAB32123.1;
EMBL; X52959; CAA37132.1;
EMBL; X56502; CAA39857.1;
EMBL; L15619; AAA40928.1;
EMBL; X56503; CAA39858.1;
EMBL; M98450; AAA91892.1;
EMBL; M59458; AAA48692.1;
PIR; A35554; A35554.
PIR; A39459; A39459.
PIR; A60651; A60651.
PIR; C38611; C38611.
PIR; S05016; S05016.
PIR; S12737; S12737.
PIR; S14478; S14478.
PIR; S14511; S14511.
PIR; S14724; S14724.

076485;
 15-JUL-1999 (Rel. 38, Last created)
 15-JUL-1999 (Rel. 38, Last sequence update)
 15-JUL-1999 (Rel. 38, Last annotation update)
 CASEIN KINASE II BETA CHAIN (CK II) (EC 2.7.1.37).
 Spodoptera frugiperda (fall armyworm).
 Cukaryota; Metazoa; Arthropoda; Insecta; Diptera;
 Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.
 (1)
 SEQUENCE FROM N.A.
 Ebel W., Stepienwski A., Robertson N.M., Alnemri E.S., Litwack G.;
 "Identification, cloning and expression of Spodoptera frugiperda
 casein kinase II";
 Submitted (JUN-1998) to the EMBL/GenBank/CDK databases.
 CC -!- FUNCTION: PLAYS A COMPLEX ROLE IN REGULATING THE BASAL CATALYTIC
 CC ACTIVITY OF THE ALPHA SUBUNIT (BY SIMILARITY).
 CC -!- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS.
 CC -!- DEVELOPMENTAL STAGE: ELEVATED LEVELS OF CKII ARE OBSERVED DURING
 CC EMBRYOGENESIS, LIVER REGENERATION, AND ADIPOCYTE DIFFERENTIATION.
 CC -!- PTM: PHOSPHORYLATED BY ALPHA CHAIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE CASEIN KINASE 2 BETA CHAIN FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AF071211; AAC24042.1; -;
 DR INTERPRO; IPR000704; -;
 DR PFAM; PF01214; CK_II_beta; -;
 DR PRINTS; PR00472; CASKINASE11.
 DR PROSITE; PS01101; CK2_BETA; 1.
 DR TRANSFERASE; Serine/threonine-protein kinase; Phosphorylation.
 DR MOD_RES; 2 2 PHOSPHORYLATION (AUTO-) (PROBABLE).
 DR DOMAIN; 55 64 ASP/GIU-RICH (ACIDIC).
 DR SEQUENCE; 221 AA; 25376 MW; 3317HR351D708536 CRC64;
 Query Match 39.8%; Score 592; DB 1; Length 221;
 Best Local Similarity 52.6%; Pred. No. 3.2e-43;
 Matches 101; Conservative 36; Mismatches 55; Indels 0; Gaps 0;
 Y 83 SEGDDTSWISWFCNLRGNDFCEVDEDIQDDFNLCGLSGOVYKYALDLILDVDSNS 242
 2 SSSSEVSWISWFCNLRGNDFCEVDEDIQDDFNLCGLSGOVYKYALDLILDVDSNS 61
 143 EMFTDQHEWVESAAEMLYGLIHVRYILTCKMAAMTEKYKNCDFGRCPVFCGQSCIP 202
 62 LDNPQNSDLVEQASFLXGLIHARYILNRRGSGUMLEKFAQDFGHCPRVYCECCPMLP 121
 203 VGSDDTIPRSTVKIYCKEDISYPRSKFGQGNIDGAYFGTTPPHLFLMTYGNLKPQKPTQ 262
 122 LGLSDVPGAMVKLYCPRCMDVYTPKSSRHHHTDGAFTGTFPMVFMVHPYRKRKRPAS 181
 263 SYVVKPIFGFKVH 274
 182 QVFRLYGFKIH 193
 RESULT 11
 C22B_CAEEL STANDARD; PRI: 234 AA.
 D F28548; C62352; Q22077;
 C 01-DEC-1992 (Rel. 24, Created)
 T 01-DEC-1992 (Rel. 24, Last sequence update)
 T 15-JUL-1999 (Rel. 38, Last annotation update)
 E CASEIN KINASE II BETA CHAIN (CK II) (EC 2.7.1.37).
 N KIN-5 OR KIN-10 OR T01G9.6.
 N Caenorhabditis elegans.
 C Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 C Rhabditidae; Telodoridae; Caenorhabditis.

RN SEQUENCE FROM N.A.
 RP MEDLINE; 92011787.
 RA Hu E., Rubin C.S.;
 RT "Casein kinase II from Caenorhabditis elegans. Cloning,
 RT characterization, and developmental regulation of the gene encoding
 RT the beta subunit";
 RL J. Biol. Chem. 266:19796-19802(1991).
 (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Lennard N.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/CDK databases.
 CC -!- FUNCTION: PLAYS A COMPLEX ROLE IN REGULATING THE BASAL CATALYTIC
 CC ACTIVITY OF THE ALPHA SUBUNIT (BY SIMILARITY).
 CC -!- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS.
 CC -!- DEVELOPMENTAL STAGE: ELEVATED LEVELS OF CKII ARE OBSERVED DURING
 CC EMBRYOGENESIS, LIVER REGENERATION, AND ADIPOCYTE DIFFERENTIATION.
 CC -!- PTM: PHOSPHORYLATED BY ALPHA CHAIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE CASEIN KINASE 2 BETA CHAIN FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; M73827; AAA27983.1; -;
 DR EMBL; Z75713; CAB00056.1; -;
 DR EMBL; Z75713; CAB00053.1; -;
 DR PIR; A41036; A41036.
 DR WORMPEP; T0169.6A; CE18168.
 DR WORMPEP; T0169.6B; CE06343.
 DR INTERPRO; IPR000704; -;
 DR PFAM; PF01214; CK_II_beta; 1.
 DR PRINTS; PR00472; CASKINASE11.
 DR PROSITE; PS01101; CK2_BETA; 1.
 DR TRANSFERASE; Serine/threonine-protein kinase; Phosphorylation;
 KW Alternative splicing.
 KW MOD_RES; 2 2 PHOSPHORYLATION (AUTO-) (PROBABLE).
 FT DOMAIN; 55 63 ASP/GIU-RICH (ACIDIC).
 FT VARSPIC; 58 58 P -> PE (IN ISOFORM B).
 FT CONFLICT; 141 141 M -> D (IN REF. 2).
 SQ SEQUENCE; 234 AA; 26452 MW; A0814A48B768347D CRC64;
 Query Match 39.6%; Score 588.5; DB 1; Length 234;
 Best Local Similarity 53.3%; Pred. No. 6.7e-43;
 Matches 104; Conservative 36; Mismatches 48; Indels 7; Gaps 2;
 QY 83 SEGDDTSWISWFCNLRGNDFCEVDEDIQDDFNLCGLSGOVYKYALDLILDV---DA 139
 D 2 SSSSEVSWISWFCNLRGNDFCEVDEDIQDDFNLCGLSGOVYKYALDLILDVDD 61
 QY 140 SENSEFTDQHEWVESAAEMLYGLIHVRYILTCKMAAMTEKYKNCDFGRCPVFCGQSQS 199
 D 62 EDNAINTD----LVEQAAEMLYGLIHARYILNRRGSGUMLEKFAQDFGHCPRVYCECCP 117
 QY 200 CLPVGQSDIPRSTVKIYCKEDISYPRSKFGQGNIDGAYFGTTPPHLFLMTYGNLKPQK 259
 D 118 MLPGLSDVPGAMVKLYCPRCMDVYTPKSSRHHHTDGAFTGTFPMVFMVHPYRKRKRP 177
 QY 260 PTQSYVVKPIFGFKVH 274
 D 178 PVIQVVKLYGFKIH 192
 RESULT 12
 KC2C_DROME STANDARD; PRI: 219 AA.
 I5 KC2C_DROME
 AC Q96863; Q9V919;

15-JUL-1999 (Rel. 38, Created)
 15-JUL-1999 (Rel. 38, Last sequence update)
 01-OCT-2000 (Rel. 40, Last annotation update)
 CASEIN KINASE II BETA' CHAIN (CK II) (EC 2.7.1.37).
 CKII-BETA2.
 Drosophila melanogaster (fruit fly).
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 [1]
 SEQUENCE FROM N.A.
 Bidwai A.P., Zhao W., Glover C.V.C.;
 "A gene located at 56F1-2 in *Drosophila melanogaster* encodes a novel
 metazoan beta-like subunit of casein kinase II";
 Mol. Cell Biol. Res. Comm.n. 1:21-28(1999).
 [2]
 SEQUENCE FROM N.A.
 STRAIN-BERKELEY;
 MEDLINE: 20196006.
 Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.C., Hest G., Nelson C.R., Miklos G.L.G.,
 Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Boishakov S.,
 Borkova D., Botchan M.R., Bouck J., Brockstein P., Brottier P.,
 Hurlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K.J., Dong L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
 Foster C., Gabriele A.E., Garg N.S., Gelbart W.M., Glessner K.,
 Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.F., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,
 Jalili M., Kalush F., Karpen G.H., Ke Z., Kennison C.A., Ketchum K.A.,
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
 Lasko P., Lei Y., Levitsky A., Li J., Li Z., Liang Y., Lin X.,
 Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson P.,
 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 Mount S.M., Moy M., Murphy R., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclik J.M.,
 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 Shue B.C., Steden-Kiamos I., Simpson M., Skupski M.P., Smith I.,
 Spier E., Spradling A.C., Stapleton M., Strong R., Sun H.,
 Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 Ye J., Yeh R.F., Zaveri J.S., Zhao M., Zhang G., Zhao C., Zheng L.,
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 Gibbs R.A., Myers E.W., Rubin G.M., Venter C.C.;
 "The genome sequence of *Drosophila melanogaster*";
 Science 287:2185-2195(2000).
 -!- FUNCTION: PLAYS A COMPLEX ROLE IN REGULATING THE BASAL CATALYTIC
 ACTIVITY OF THE ALPHA SUBUNIT.
 -!- SUBUNIT: TRIMER OF TWO ALPHA AND TWO BETA' CHAINS.
 -!- PTM: PHOSPHORYLATED BY ALPHA CHAIN (BY SIMILARITY).
 -!- SIMILARITY: BELONGS TO THE CASEIN KINASE 2 BETA' CHAIN FAMILY.

 This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

 EMBL; U51209; AA000080.1;
 EMBL; AE003792; AAF57483.1; .

LYBASE; FB00026136; CKII-Beta2.
 INTERPRO: IP0000704; .
 PFAM: PF012144; CK_II_beta; .
 PRINTS: PR00472; CASRKINASEII.
 PROSITE: PS01101; CK2_BETA; 1.
 TRANSFERASE; Serine/threonine-protein kinase; Phosphorylation.
 MOL.MES 2 2 PHOSPHORYLATION (AUTO-) (PROBABLE).
 DOMAIN 63 71 ASP/GLU-RICH (ACIDIC).
 SEQUENCE 219 AA; 24966 MW; E43E80AA465D8666 CRC64;
 Query Match 36.2%; Score 538; DB 1; Length 219;
 Best Local Similarity 48.4%; Pred. No. 1.2e-38;
 Matches 93; Conservative 37; Mismatches 60; Indels 2; Gaps 2;
 QY 83 SEGDDTSWISWFCNLKRGDFFCEVDEYDQDDNLCGLSGQVPPYDYALDILDVDASNS 142
 DB 2 TDSDESSIIHWFCQKRGNEFFCEVDEYDQDDNLCGLSGQVPPYDYALDILDVDASNS 61
 QY 143 ENFTDQHEWVESAAEMLYGLIHVRYLTITKGNAAATEKYKNCDFGRCPRVFCGSGCLP 202
 DB 62 S--EDPAEPLEASAEKLYGLIHARFILNRGIELMDKYNGKGFCTCFACFUSQVLP 119
 QY 203 VGSDDIPRSSTVVIYCPKCEDISYPSKFGNIDGAYFGTTPHFLMTYGNLKPQKPTQ 262
 DB 120 IGLSDNFGEDWRIYCPKNDVYIPKASRHSNLDGAFGTFGPHMFMEKPDARPKRAQ 179
 QY 263 SYVPKTFGPKVH 274
 DB 180 KVPRLYGFKIH 191
 RESULT 13
 KC2C_YEAST STANDARD; PRT: 258 AA.
 ID KC2C_YEAST
 AC P38930;
 DI 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE CASEIN KINASE II BETA' CHAIN (CK II) (EC 2.7.1.37).
 GN CKB2 OR YOR039W OR OR26.32.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomycetes.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94299539.
 RA Reed J.C., Bidwai A.P., Glover C.V.C.;
 "Cloning and disruption of CKB2, the gene encoding the 32-kDa
 regulatory beta'-subunit of Saccharomyces cerevisiae casein kinase
 II";
 J. Biol. Chem. 269:18192-18200(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC S-RAIN-S288C / FY1679;
 RA de Haan M., Mease A.C., Grivell L.A.;
 Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Landt O., Hiesel R., Unseld M.;
 Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 172-258 FROM N.A.
 RC STRAIN-AP3;
 RA Halder M., Bito A., Wallner J., Breitenbach M.;
 Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP PARTIAL SEQUENCE.
 RX MEDLINE: 94182950.
 RA Bidwai A.P., Reed J.C., Glover C.V.C.;
 "Casein kinase II of Saccharomyces cerevisiae contains two distinct
 regulatory subunits, beta and beta'";
 Arch. Biochem. Biophys. 309:348-355(1994).
 RL

-!- FUNCTION: PLAYS A COMPLEX ROLE IN REGULATING THE BASAL CATALYTIC
 ACTIVITY OF THE ALPHA SUBUNIT (BY SIMILARITY).
 -!- SUBUNIT: TETRAMER COMPOSED OF AN ALPHA CHAIN, AN ALPHA', ONE
 BETA CHAIN AND ONE BETA' CHAIN.
 -!- PTM: PHOSPHORYLATED BY ALPHA CHAIN (BY SIMILARITY).
 -!- PTM: THE N-TERMINUS IS BLOCKED.
 -!- SIMILARITY: BELONGS TO THE CASEIN KINASE 2 BETA CHAIN FAMILY.

This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

EMBL: U08849; AA21856.1;
 EMBL: X87331; CAAG6758.1;
 EMBL: X74947; CAA59229.1;
 EMBL: X82893; CAA58064.1;
 SGD: S0003565; CKR2.
 INTERPRO: IPR000704;
 Pfam: PF01214; CK_II_beta.1.
 PRINTS: PR00472; CASNKINASEII.
 PROSITE: PS01101; CK2_BETA.1.
 Transferrase: Serine/threonine-protein kinase: Phosphorylation.
 SEQUENCE 258 AA; 29842 MW; D6060C93C70B19A4 CRC64.

Query Match 34.6%; Score 514.5; DB 1; Length 258;
 Best Local Similarity 46.0%; Pred. No. 1.4e-36;
 Matches 99; Conservative 35; Mismatches 74; Indels 7; Gaps 2;
 62 IKTLQPDVSESDTSRGSYSGSGDDTSISNFCNLKNGDNFFCEVDEVIQDQFNLCGLS 121
 16 SRVQDQVLMDDSDSRV-----DKWIDIFLGRKGHEFYCDVDFEYITDFENLNNQ 69
 122 GQVPPYYAYALDIL--DVDASNSIMFTDEQHEMVESAAMEYGLIHRVYILITKGMAANPE 180
 70 KTVSKESYVVYVIVDLDSDSIENTHALEQENSRKLYGLIHKRYII--KGLQKMYA 129
 181 KYKNCFDGRCPVFCGQSCFLVGSQDIPRSSTVKIYCKCEDISYPSKPGQNGIDGYF 240
 130 KYKEADFGCRPVYCNLOQLVGLHDLPGIDCVKLYCSQEDIAVPSKSRSSIDGYF 189
 241 GTTFPLELMTGNLKPQKPTGQSYVZPKIEGFVHK 275
 190 G-SFGQMFLOAPQPMVPRKPTKRYVPRKIFGFLHK 224

RESULT 14
 22B_YEAST
 ID KC2B_YEAST STANDARD; PRT; 278 AA.
 AC P43639;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE CASEIN KINASE II BETA CHAIN (CK II) (EC 2.7.1.37).
 GN CKB1 CR YGL015W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 CC Saccharomycetaceae; Saccharomycetes.
 RP
 RN
 RP SEQUENCE FROM N.A.
 RA STRAIN=S288C;
 MEDLINE: 93256195.
 AB Bidwai A.P., Reed J.C., Glover C.V.C.:
 "Cloning and disruption of CKB1, the gene encoding the 38-kDa beta
 subunit of Saccharomyces cerevisiae casein kinase II (CKII). Deletion
 of CKII regulatory subunits elicits a salt-sensitive phenotype".
 J. Biol. Chem. 270:10395-10404(1995).
 [2]
 RP SEQUENCE FROM N.A.

RA Hebling U., Hofmann B., Delius H.;
 Submitted (May-1996) to the EMBL/GenBank/DBJ databases
 CC -!- FUNCTION: PLAYS A COMPLEX ROLE IN REGULATING THE BASAL CATALYTIC
 ACTIVITY OF THE ALPHA SUBUNIT (BY SIMILARITY).
 CC -!- SUBUNIT: TETRAMER COMPOSED OF AN ALPHA CHAIN, AN ALPHA', ONE
 BETA CHAIN AND ONE BETA' CHAIN.
 CC -!- PTM: PHOSPHORYLATED BY ALPHA CHAIN (BY SIMILARITY).
 CC -!- PTM: THE N-TERMINUS IS BLOCKED.
 CC -!- SIMILARITY: BELONGS TO THE CASEIN KINASE 2 BETA CHAIN FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

Query Match 30.3%; Score 446; DB 1; Length 278;
 Best Local Similarity 38.4%; Pred. No. 9.5e-31;
 Matches 89; Conservative 47; Mismatches 58; Indels 38; Gaps 4;
 QY 81 SGSEGGDTS-----WISNFCNLKNGDNFFCEVDEYIQQDQFNLCGLSGVPPYVDALDIL 135
 DB 12 TGSDDSSGAYDEWIPSCSRFGHEFYCQVTFEEDFNMTLSLQEVPIRYKALDIL 71
 QY 136 DVDAS-----NSPMFTDEQHE-----MVESAAMEYGLI 165
 DB 72 DLEANSDEEDEDVDEVDQENQSDGHDGKRNKSPVNVKSIIIEUAEOYGLI 131
 QY 166 VRYLTITKGMAAMEKYKNCDFGRCPVFCGQSCFLVGSQDIPRSSTVKIYCKCEDIS 225
 DB 142 ARFILTLPGLQAMAEEKDHEKFGTCPRYVCNGMOILPGCLSDITVGHKHTVRLYCPSCQDLY 191
 QY 226 YPSKFGQNGIDGAVFGITFPLELMTGNLKNK---PQPTOSYVPRKIEGFVH 274
 DB 192 LPQSSRFCLLEGAPWGTSFPGVFLKHFKELEYVERKSKESTELKVFGRIN 243

RESULT 15
 KC2B_CANAL
 ID KC2B_CANAL STANDARD; PRT; 294 AA.
 AC Q59906;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE CASEIN KINASE II BETA CHAIN (CK II) (EC 2.7.1.37).
 GN CKB1.
 OS Candida albicans (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 CC anamorphic Saccharomycetales; Candida.
 RP
 RN
 RP SEQUENCE FROM N.A.
 RA Waiz K., Pardo P.S., Passeron S.:
 "Complete sequence of the protein kinase CK2 beta subunit gene from
 Candida albicans (CaCKB1)".
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP CHARACTERIZATION
 RC STRAIN=ATCC 64385 / i001;
 RX MEDLINE: 97288362.
 RA Waiz K., Pardo P.S., Passeron S.:
 "Purification and characterization of protein kinase CK2 from Candida

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

M nucleic - nucleic search, using sw mode.

Run on: November 15, 2000, 11:23:49 : Search time 1249.31 Seconds
(without alignments)
3775.673 Million cell updates/sec

Title: US-09-359-026-1
Perfect score: 1080
Sequence: 1 gtcgaccacgcgtccgaga.....tggagcacaacacaccatt 1380

Scoring table: IDENTITY_NIC
Gapop 10.0 , Gapext 1.0

Searched: 1033670 seqs, 2:83789503 residues 2057340
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

- GenBank: 1: gb_ba1.* 2: gb_ba2.* 3: gb_cm.* 4: gb_ov.* 5: gb_pat.* 6: gb_ph.* 7: gb_pl1.* 8: gb_pl2.* 9: gb_pl3.* 10: gb_pr2.* 11: gb_pr3.* 12: gb_ro.* 13: gb_sy.* 14: gb_un.* 15: em_fun.* 16: em_hum1.* 17: em_hum2.* 18: em_in.* 19: em_or.* 20: em_ov.* 21: em_ov.* 22: em_pat.* 23: em_ph.* 24: em_pl.* 25: em_ro.* 26: em_sy.* 27: em_sy.* 28: em_un.* 29: em_vl.* 30: gb_ba1.* 31: gb_in1.* 32: gb_in2.* 33: gb_in3.* 34: gb_pl3.* 35: gb_pl4.* 36: em_bal.* 37: em_ba2.* 38: em_htg1.* 39: em_htg2.* 40: em_htg3.* 41: em_htg4.* 42: em_htg5.* 43: em_htg6.*

- 44: em_htg7.* 45: em_htg8.* 46: em_htg9.* 47: em_htg10.* 48: em_htg11.* 49: em_htg12.* 50: em_htg13.* 51: em_htg14.* 52: em_htg15.* 53: em_htg16.* 54: em_htg17.* 55: em_htg18.* 56: em_htg19.* 57: em_htg20.* 58: em_htg21.* 59: em_htg22.* 60: em_htg23.* 61: em_hum3.* 62: em_hum4.* 63: em_hum5.* 64: em_hum6.* 65: gb_pr5.* 66: gb_pr6.* 67: gb_pr7.* 68: gb_htg.* 69: gb_htg2.* 70: gb_htg3.* 71: gb_htg4.* 72: gb_htg5.* 73: gb_htg6.* 74: gb_htg7.* 75: gb_htg8.* 76: gb_htg9.* 77: gb_htg10.* 78: gb_htg11.* 79: gb_htg12.* 80: gb_htg13.* 81: gb_htg14.* 82: gb_htg15.* 83: gb_htg16.* 84: gb_htg17.* 85: gb_htg18.* 86: gb_htg19.* 87: gb_htg20.* 88: gb_htg21.* 89: gb_htg22.* 90: gb_htg23.* 91: gb_sts1.* 92: gb_sts2.* 93: gb_vil.* 94: gb_vil2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %				DB ID	Description
	Score	Match	Length			
1	1080	100.0	1080	7	AF068318	AF068318 Arabidops
2	605	56.0	88548	6	AF2727H5	AL163852 Arabidops
3	591.4	54.8	10989	7	AF263518	AF263518 Arabidops
4	413.2	38.3	1285	8	ATHCKIB	L22563 Arabidops
5	390.6	36.2	1229	8	ATU03984	U03984 Arabidops
6	245.6	22.7	86033	7	AC003672	AC003672 Arabidops
7	204.4	18.9	648	4	XLCKIIB	X62376 X.lacvis mR
8	201.2	18.6	1677	4	S76877	S76877 casein kina
9	198	18.3	1645	4	AF133088	AF133088 Cyprinus
10	183	16.9	914	12	MMCKIIB	X52959 Mouse mRNA
11	183	16.9	944	12	MMCKIIBH	X56502 Mouse CK11
12	182	16.9	521	66	HSCK11	X16312 Human mRNA


```

RRPSNVAQDUKRWTKNGSLPAGYQGNVQFRPGGGNSGVLPNPMHQGPTISRPWQVPG
PMWGMRNIPLEKWRGNSNFOQAGLPPSPHTPMGVNHAERKYOVCITADEEAKOM
OLKSLINKLIPONEKLEKLEQVKSVNIONAVTLSCVLSCEKA.MEPTCEMVADGCE
ELSGALPDPNENGK-ITFR..LLNKUEFERKEKEEENSKVAFPOQVCTEEDRE
KELVVRMLGNIRLIGLKKRMLTEKIMHACOKLLGYNOOPHEENIEALCKLMST
TCVLDHNKAFQMDGVFEKMKLSCKOFISSRVFMLINAIID.RKNKWFRRMKVGP
KKTEVHRDAAEKFOIQANRLSRGPMKSSORRHMPFSSRPGGGMLSPPAOMGSGY
HGPGUGRSNODLREDRPSYFRRMVPIDORSVCEPITLGPQGLGOGMSIRRPV
ASN-YQDAIANGGDSRRPAGLNGSGSHRPPSPVTHGRSSRQEKCTAVHREFASL
SRASDSEVSARQVLOGPSATVNSPERNALSBEQLENLSLAKKEYYSARQENELG
MKMDMNSPAPHPNLSLUMWTSDFERKDEKDLAKLLNVLKSDNALNLEVDLVKGF
ESVLTKEVDYNDAPKAAPFSGRFGKSVTEKVVLTIGRLIQEGEESPSLIFPOL
GGDVIGSVLENKTEAGBEIIVEIRRSSENEEGTAYGASIRKQKKMEVSQHSKYF
GPFQGYGVKKVKGWIGCKDCKGKVGKAGGATMNTASAVTVRSIRKLKQIEG"
39450..39540
/gene="P27H5_30"
/number=1
exon 39541..42284
/gene="P27H5_30"
/number=2
intron 42285..42683
/gene="P27H5_30"
/number=2
exon 42684..42878
/gene="P27H5_30"
/number=3
intron 42879..42964
/gene="P27H5_30"
/number=3
exon 42965..43227
/gene="P27H5_30"
/number=4
intron 43228..44008
/gene="P27H5_30"
/number=4
exon 44009..44026
/gene="P27H5_30"
/number=5
intron 44027..44420
/gene="P27H5_30"
/number=5
exon 44321..44409
/gene="P27H5_30"
/number=6
intron 44410..44507
/gene="P27H5_30"
/number=6
exon 44508..44590
/gene="P27H5_30"
/number=7
intron 44591..44686
/gene="P27H5_30"
/number=7
exon 44687..44750
/gene="P27H5_30"
/number=8
gene 45714..46362
/gene="P27H5_40"
gene complement(join(45714..45844,45993..46158,46255..46364,
46453..46671,46738..46962))
/gene="P27H5_40"
exon complement(45714..45844)
/gene="P27H5_40"
CDS
complement(join(45714..45844,45993..46158,46255..46364,
46453..46671,46738..46962))
/codon_start=1
/product="regulatory subunit of protein kinase CK2"
/protein_id="CA887862.1"
/db_xref="GI:7576201"
/translation="MYKENSGGGGGSRSEI:GGAIIDRRKINDALNKKLAKSSSTSTT
TSRVFSSKDKDPFSTSTKTLQFDVESETDSRSDVSGSEGDTSWISWFCNLRGNDF

```

```

Query Match 56.0%: Score 605; DB 8; Length 88548;
Best Local Similarity 71.88; Pred. No. 2.4e-140;
Matches 1063; Conservative 0; Mismatches 0; Indels 418; Gaps 4;

Cy 18 agagaaagaaacccctagattctccggtctctctctctctctctctctctctctctctcaagctctcaga 77
Db 47086 AGAAGAAACCCCTAGATTCTCCGTCCTCTCTAAATTCCTTCTCTCAAGCTCTCAGA 47027

Cy 78 aactctagacactcttogagaalctaatactccaaatllclclctctcttttggaaaaaggaatcg 137
Db 47026 AAGTCTACACTTTCGAGAATCTAATCTCCAAATTTCTTGCTTTTGGAGAAAGGAATCG 46967

Cy 138 aattatatacaagaacgctagtgagagagtggtggtggtggtggtggtggtggtggtggtggtggt 197
Db 46966 AATTATGTACAGAAACGTAGTGGAGGAGGGTGGTGGGGTGGTGGGGTGGTGGGGTGGTGGGGT 45907

Cy 198 cggtyggagctattgatcggaacgaatacaacgatgcactcaataagaactagagaaatc 257
Db 46906 CGGTGGAGCTATTGATCGAAACGAATCAACGATGCCTCAATAAGAAACTAGAGAAATC 46847

Cy 258 tteaacttcaacacacacatctagggllttctctcttaagacaaagatcccttllcctt 317
Db 46846 TCAACTTCCACCACCATCTAGGGTTTCTCTCTTAAAGACAAAGATCCCTTTTCCTT 46787

Cy 318 caeatctactaaaaactcagcttctctgat 345
Db 46786 CACATCTACTAAACTCAGCTTCTGATGGTITGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 46727

Cy 346 -----gtggaa 351
Db 46726 CTTTITGTTGTTAATTCCTTCTCTGATGATTTTITTTTGGTGTGTCAGTGGAA 46667

Cy 352 tcggaactgatagtgagggtctgatgtgagtgagtcgagaggtgatatacgcgcgtgg 411
Db 46666 TCGGAAACTGATAGTGAAGGCTCTGATGIGAGTGGATCGGAGGCTGATAGCTGCTGTGG 46607

Cy 412 atctcttggttttgaatttgagaggaatgattctctctggaagtcgatgaagattat 471
Db 46606 ATCTCTGTTTGTAAATTGAGAGGGAATGATTCTTCTGTAAGTCGATGAAGATTAT 46547

Cy 472 attcaagatgatttcaatctcttgggttaagtggttcaagtcctctctctctctctctctctctct 531
Db 46546 ATTCAAGATGATTCAATCTTTGTTGGTTAAGTGGTCAAGTCCCTTACTATGATTATGCA 46487

Cy 532 ctgcactcattttagatgttgaagtcctcaaa 565
Db 46486 CTGATCTCATTTTAGAIGTGTATGCTTCCAAACAGTAAGTCATCTCTCTCTCTCTCTCTCTCTCT 46427

Cy 565 ----- 565
Db 46426 TTTCTTTTGTTAATAAGGAGCTAGTAAAGTTTGGTCTGAAAATCTGTATCTTAIGTTT 46367

Cy 566 ---gtgagactgttactatgaacagcatgaatggttggaatcagctgtgagatgcata 623
Db 46366 AGCTGAGATGTTTACTGATGAACAGCATGAATGCTGGAATCAGCTGCTGAGATGCTATA 46307

Cy 624 tggcttallcatgttcgttacattllgactactaaaggaalqactcaat 674
Db 46306 TGGCTTATTCACTGCTTACATTTGACIACIACIACIACIACIACIACIACIACIACIACIACI 46247

Cy 675 ----- 674
Db 46246 GAGAACTCTCTACTCTTTTGTATGTTTTTGGTGGCTTTTAGCTTCGTTATTTGATTAAAC 46187

Cy 675 -----gactgagaagtaagaactgtgatttcggagag 707
Db 46186 GACGCTCTTCTTTATTGATCTCTGATAGCTGAGAAGTACAAAGAACTGTGATTTTCGGGAG 46127

Cy 708 atgcccagagatttctcttcggtcagctcttctctccagttggacaatccgatatccc 767
Db 46126 ATGCCCGAGAGTTTCTGTTGCGGTCACTTGTCTCCAGTTGGACAATCCGATATCCC 46067

```


b 9437 ATTCACATGATTTCAATCTTTCTGCTTAAAGTCTCAATCTCTACTATATATATATCA 9378
 j 532 ctggatctcatcttagatgttgatgcttccacaa 565
 b 9377 CTTCATCTCACTTACATGTTGATGCTTCCACAGTAACTCATCTCTCTCTCTCTCTC 9318
 y 566 ----- 565
 d 9317 TTTCTTTTGTGTAATAAGAGCTATGAAGTTCTGTCGAACTCTTGATCTATCTATCTT 9258
 y 566 -gtgaagatcttaactgatgaacagatgaataggtggaactgagctgctgagctgata 623
 b 9257 AGTGAGATCTTACCTGATGACAGAGTAACTGATGCTGCTGCTGCTGCTGCTGCTGCT 9193
 y 624 tggcttattacatgttggtttacatttttactactactaagaagaaagctgcaat 674
 b 9197 TGGCTCTTCACTCTCTGCTTACATTTTGACTACTAAGGAATGGCTCCAACTGTTAGTTA 9138
 y 675 ----- 674
 j 9137 GAGAAATCTCTACTCTCTTTGTTTATGCTTTTGGCTCTTGGCTCTTGGCTCTTGGCTCTT 9078
 675 ----- gactggaagatcaacaaactgtgattccggag 757
 b 9077 GAGCTCTCTGTTTATGATCTCTGATAGCTGAGAGTACAGAACTGGATTCGGGAG 9018
 y 708 atgcccagaggttttctgttgagctgagctcttctctccagttggagcaatccgatactcc 767
 b 9017 ATGCCGAGAGCTTCTGTTGCGGCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 9958
 y 768 gaggctgaactgtgaagatatactacccctaaatgcgaggaatatactta-cccccgat 826
 b 8957 GAGATCAGTACTGCTGAGATATACTGCCCTAAATCGGAGCATATATCTTACCCCGCAT 8898
 y 927 ctataatccagggca----- 841
 b 8897 CTAAATTCGAAGGCGATGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8836
 y 842 ----- 841
 b 8837 TTTCAATATTCAGTGAAAGCTTAGTCTGATTTTGGTTGAGTGGACACCTCTGATCTT 8778
 y 842 -----atattgatggagcga 857
 b 8777 GAGTGTCTATCTTAGCTTTTCTTAAATGACCTGTGCGAGATTTGATGAGCGCTA 8718
 y 858 ctgtggaacacatctccctcactgttctctgagacttaccggaacttaagccgcagaa 917
 b 8717 CTTTGGAACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8658
 y 918 gcttactcaagcctatgtcccaaaaactcttctgttctgaggtacacaaatgatacta 977
 b 8657 CCTACTCAAGCTATGTCCCAAAATCTCTGGCTCAAGGACACAAACCTGATCTA 8598
 y 978 ctgctctgacttctccaggttgatgatactttagtctgctctgactgctgagatagca 1037
 b 8597 CTGCTCTGCTCACTCTCAATGGGATGATACATTTAGTGGCTCTGTAAATGCAATCCGATGACCA 8538
 y 1038 actaaacatgagctgaggtgaactggaacatatacaaccatt 1080
 y 8537 ACTGAACGATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8495
 RESULT 4
 THCK1B
 XUS ARCK1B 1285 bp mRNA PLN 18-NOV-1994
 DEFINITION Arabidopsis thaliana casein kinase II beta subunit CK31 mRNA,
 complete cds.
 VERSION L22563
 accession L22563.1 GI:468263
 SYMBOLS thale cress.
 SOURCE Arabidopsis thaliana
 ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 Brassicales; Brassicaceae; Arabidopsi.
 1 (bases 1 to 1285)
 Collinge,M.A. and Walker,J.C.
 Isolation of an Arabidopsis thaliana casein kinase II beta subunit
 by complementation in Saccharomyces cerevisiae
 Plant Mol. Biol. 25 (4), 649-658 (1994)
 94339478
 2 (bases 1 to 1285)
 Collinge,M.A.
 Direct Submission
 Submitted (01-APR-1994) Margaret A. Collinge, Division of
 Biological Sciences, University of Missouri-Columbia, 110 Tucker
 Hall, Columbia, MO 65211, USA
 Location/Qualifiers
 1. 1285
 /organism="Arabidopsis thaliana"
 /db_xref="taxon:3702"
 141..1004
 /codon_start=1
 /product="casein kinase II beta subunit CKB1"
 /protein_id="AA53233.1"
 /db_xref="GI:468264"
 /translation="MYDRGVNSRPRVVDKRINDALERSPSSTSRVNGKGTVT
 AATTNLIKQCSNNINHRDSASLSKNVTSDSDSDTDESDVSQSGEDTSMI
 SWFCNLGNRFCEYVDYDQIDUPNLCGLSSLPVYAYALDILLVSSQSGEMFTSRQ
 NELIESAAEMLYGLIHARYILTSKLAAMDLYKNTDFRCPRVCCGQCPVQSD
 LPRSSVIKYPKCEDIYPRSKYQGNIDGAYGFTTFPHLFMTYGLHLPKAKATQNYV
 QRVFGFKLHP"
 BASE COUNT 405 a 239 c 292 g 349 t
 ORIGIN
 Query Match 38.3% Score 413.2; DB 8; Length 1285;
 Best Local Similarity 76.7%; Pred. No. 1.3e-92;
 Matches 505; Conservative 0; Mismatches 153; Indels 0; Gaps 0;
 Oy 322 totactaaactcagcttcctgagtggaatcgaaactgataatgaaggtctgagtg 381
 Db 354 TCGAAGACAATACGGTTTCGTGATGATGATGATGATGATGATGATGATGATGATG 413
 Oy 382 agtgcacagtcctgagtgatgacgtcggtggtctcttgggttctgaaatttgagaggaat 441
 Db 414 AGTGGTCTGATGAGAGGACACTTTCATGGATATCTTGGTTTTCATCTAAGAGGAAC 473
 Oy 442 gattctctctggaagtcgaggaattattcaagatgattcaactcttgggttta 501
 Db 474 GAGTCTTTTGTGAAGTTGATGATGATGATGATGATGATGATGATGATGATGATG 533
 Oy 502 agtgcacagtcctgagtgatgattgattgattgattgattgattgattgattgattgatt 561
 Db 534 AGCACTCTAGTTCCTCTACTAGAGTACGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 593
 Oy 562 aacagtgagatglttactgag 621
 Db 594 CAAGGAGAGATGTTTACAGAGGACAGAAATGAATGATGATGATGATGATGATGATGATG 653
 Oy 622 taagtctatttactgcttctgcttctgcttctgcttctgcttctgcttctgcttctgctt 661
 Db 654 TATGAGTATGATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 713
 Oy 682 aggtacaaagaaactgtgatttcggggagagagagagagagagagagagagagagagag 741
 Db 714 AATACAAAAAATAAGACTTTGGAAGATGTCCAAGAGTTTATTCCTGTGGCCAACTTGT 773
 Oy 742 ctccagtgaggacaatccgagatcccgagatcccgagatcccgagatcccgagatcccgag 801
 Db 774 CTTCGGTGGTCAATCACTACTTACCGGATCTAGCACTGTGAAGATATATTTGCCGAAA 833
 Oy 802 tgcgaggatatacttaccgagatcccaattcccaagcaatattgatggagcgtacttt 861
 Db 834 TCGAAGACATTTATACCCAGGATCAAGGATCAAGGATCAAGGATCAAGGATCAAGGATCA 893

(ftp://arthur.epm.ornl.gov/pub/xgrabi/). Genefinder (Phil Green, University of Washington), GenScan (Chris Burge, http://genome.stanford.edu/GENSCAN.html), and NePlantGene (http://www.cds.dtu.dk/services/NetGene2/), searches of the complete sequence against a peptide database and plant EST databases at TIGR, and manual curation based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats were identified by RepeatMasker (Arlan Smit, http://ftp.genome.washington.edu/RM/RepeatMasker.html). Genes are numbered from the top to bottom of the chromosome.

We thank the CSHL/Mashu/ARI consortium for sequencing PAC clones F6P23, F5J6, I17A9, and T13J26, the ESSA group for sequencing clone F1304, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Iabata for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especially Tixit Zhou, Hanif Khaliq, Michael E. Kearney, Lily Fu, Peng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and database support.

This work was supported by the National Science Foundation, Department of Energy and the US Department of Agriculture.

Address all correspondence to: atetigr.org.

FEATURES	source
Location/Qualifiers	
1. .86033	
/organism="Arabidopsis thaliana"	
/cultivar="Columbia"	
/db_xref="taxon:3702"	
/chromosome="11"	
<1. .299	
/note="Sequence from clone F411"	
300. .>86033	
/note="Sequence from clone F16B22"	
Join:163. .788,876. .1008,1158. .1295,1396. .1529,1651. .1776.	
2007. .2119,2200. .>2540)	
/gene="At2g44520"	
363. .>2540	
/gene="At2g44520"	
/note="F16B22.1"	
Join:469. .788,876. .1008,1158. .1295,1396. .1529,1651. .1776.	
2007. .2119,2200. .>2540)	
/gene="At2g44520"	
/codon_start=1	
/product="putative home A. tarnesyltransferase"	
/protein_id="AAC27454.2"	
/db_xref="G:598392"	
/translation="MWRKSVVTFSSRISVSSSLPNPLPWSRCLCAVNSFQPPVS ESTAKLVGTGKSEANRVEATATAATACTGTGSSRVAALAGLGHYARCYWELS KAKLSLVATSGTGLIATGNAATSPFGCGYTCAGTMMIAASANSJNQTETISNDK MRTRPLPSPGRISVPHAVAWATAGASACGLAKTMMZAAGLASNLVYAEVYT PLCK:HPITNMGAVGAIPLPLGMAASGCSYNSMLPAALYKCTDPMWALHLC RNDYAGGKMLSLHPSKRIAAVALNCHFYHPI:GFIANCERSWGLTSSWFLPESL IL:LA:AA:AFPIRDMIRKAKMFAHSLIFLPVMSGLLHRVSNNDNOQGLVEAG LTNSVSGVTKRPKRKVPVAVASAPFLPAPSEYSP Join:(4541. .4636,4771. .4947,5175. .5423,5694. .5837, 5945. .6112,6184. .6253,6334. .6415,6505. .>6679)	
/gene="At2g44530"	
<4541. .>6679	
/gene="At2g44530"	
/note="F16B22.2"	
Join:(4541. .4636,4771. .4947,5175. .5423,5694. .5837, 5945. .6112,6184. .6253,6334. .6415,6505. .>6679)	
/gene="At2g44530"	
/codon_start=1	

FEATURES	source
/product="putative phosphoribosyl pyrophosphate synthetase"	
/protein_id="AAC27455.1"	
/db_xref="GI:3341673"	
/translation="WASIPQSPPTFPALNRKSLIRPSSVRFPLKCNAAADPKFEG GNSAGPHLLIGTVPASPSRTPLSDSIYONFTRLFSTANPILAQELSCYLGDLG KIKKRFADGEIYVOLESVRCGVFIQPTCTPANENLMELLVMDACKRASAKILIT NIYIPFCYARADKTOGRSIAAKLVANLITSGADRVLACDLHSGQSGMYDIPVDH QVGVILYDILASKAISEDVVSPDGVGVARAFARAKKSDAPLAIIVDKRRHGINV AEYMNIGVQKVAIMVDMIDTAGTISKGAALLHQEGAREVYACTIHAFVSPPAIS RUSSGIFQVIITNIPLEKKNYFQITVLSVANLIGTIRVHDDCSVKT"	
complement(join(<7150. .7467,7579. .7860,7947. .8600, 8698. .>8919))	
/gene="At2g44540"	
complement(<7150. .>8919)	
/gene="At2g44540"	
/note="F16B22.3"	
complement(join(7150. .7467,7579. .7960,7947. .8600, 8698. .8919))	
/gene="At2g44540"	
/codon_start=1	
/product="putative glucanase"	
/protein_id="AAC27456.1"	
/db_xref="GI:3341674"	
/translation="MSQKNGSSQCLWTSICIVLWMSMARGAVSTNYAEALOKSLY WSNIENGSELRAHHEOGSLRAKWDYDILIRAHPOPVNYLGVGEGSDHKCWRPE FEAQRSGKLPPNOKVTRGDSALIKGSDAHDITGGYDAGDNMKFGFPLAFTTMLA DMPTRTSYRIDAQHPGSDLAGETAAMAAAS:AFAPEDKAYANILIGHAKDLFAFAK AHFGLQNSITNAGGYASSGDELLWAAALHRAINDQIYILNLTQNSGTGGPRSV AWDDKFGAQLVMALALERKVSNGKIAEYKSMARQFCNCAQKGNVNAKTPGGL LYLPMNNLOYITTAFTVLSAYSKYLEAAKASIDCPDQALQASDLQVARSQDYILG SNPKMSYMGVTNYPKPHHRAASIVSRIRKDKPTVTCGGYDKWYNPNAPNVLV GALVGGPNNDYGDERSNQQAEPATVVAPEVGLAAVF"	
complement(join(<10190. .10507,10618. .10899,10985. .11635, 11730. .>11951))	
/gene="At2g44550"	
complement(<10190. .>11951)	
/gene="At2g44550"	
/note="F16B22.4"	
complement(join(10190. .10507,10618. .10899,10985. .11635, 11730. .11951))	
/gene="At2g44550"	
/codon_start=1	
/product="putative glucanase"	
/protein_id="AAC27457.1"	
/db_xref="GI:3341675"	
/translation="MSQKNGSSQCLWTSICIVLWMSMAREAVSTNYAEALKNLLY FEAQRSGKLPPNORVTRGDSALRDGSDAHDITGGYDAGDNMKFGFPLAFTTMLA WSNIENASQLRAHHEKGNALIKLKWATDYDILIRAHPOPVNYLGVGEGSDHKCWRPE DMPTRTSYRIDAQHPGSDLAGETAAMAAAS:AFAPEDKAYANILIGHAKDLFAFAK AHFGLQNSITNAGGYASSGDELLWAAALHRAINDQIYILNLTQNSGTGGPRSV AWDDKFGAQLVMALALERKVSNGKIAEYKSMARQFCNCAQKGNVNAKTPGGL YELPMNNLOYITTAFTVLSAYSKYLEAAKASIDCPDQALQASDLQVARSQDYILG SNPKMSYMGVTNYPKPHHRAASIVSRIRKDKPTVTCGGYDKWYNPNAPNVLV GALVGGPNNDYGDERSNQQAEPATVVAPEVGLAAVF"	
complement(join(<12723. .13040,13133. .13414,13498. .14151, 14242. .>14463))	
/gene="At2g44560"	
complement(<12723. .>14463)	
/gene="At2g44560"	
/note="F16B22.5"	
complement(join(12723. .13040,13133. .13414,13498. .14151, 14242. .14463))	
/gene="At2g44560"	
/codon_start=1	
/product="putative glucanase"	
/protein_id="AAC27458.1"	
/db_xref="GI:3341676"	
/translation="MSQKNGSSQCLWTSICIVLWMSMARGAVSRNYGDALTKSLY FEAQRSGKLPSNORVTRGDSALRDGSDAHDITGGYDAGDNMKFGFPLAFTTMLA WSNIENATQLKAOEENALAKLKWATDFLIKAHPSPNVLYGVGEGSDHCKWRPE DMPTRPSYRIDAQHPGSDLAGETAAMAAAS:AFAPEDKAYANILIGHAKDLFAFAK AHFGLQNSITNAGGYASSGDELLWAAALHRAINDQIYILNLTQNSGTGGPRSV AWDDKFGAQLVMALALERKVSNGKIAEYKSMARQFCNCAQKGNVNAKTPGGL YELPMNNLOYITTAFTVLSAYSKYLEAAKASIDCPDQALQASDLQVARSQDYILG SNPKMSYMGVTNYPKPHHRAASIVSRIRKDKPTVTCGGYDKWYNPNAPNVLV GALVGGPNNDYGDERSNQQAEPATVVAPEVGLAAVF"	

Qy	595	atgtggaatcagctgtgagatgctatggtcttatttcatttcgttcaatttgaact	654
Db	48324	ATGTGTGAATCAGCTGCTGAGATGTTATATGCTTATTCATGTTGTTATATTCTCACT	48365
Qy	655	actaaagaatggctgcaat-----	674
Db	48264	ACTAAGAATGGCTGCTATGGTAAGCAAGATACCTTCTACATCTTGTTCIGATG	48205
Qy	675	-----gagtgagaagtacaagaactgtgatttcgg	704
Db	48204	ATCTTTGAATGATATCTTCTCTTTTGTAGATGGAGAAGTATRAAGATTAATGATTTCGG	48145
Qy	705	gagatgccggagagatlltctgtcggctcactctgttcttcagatgagacaatccgatat	764
Db	48444	CAGATGCCCCAGAGATTTCCTTCGCGGACAGCTGTGCTTCCTCCGTTGCCAATCTGATAT	48065
Qy	765	cccagatccagttactatgaagata;actlccctcaaatgcagagatatattctaccacg	824
Db	48084	CCGAGGTCGAGCTGTGAAGATATATCTGCCAAAATGCGAGGATATTTACTACCCCGC	48025
Qy	825	atctaaattccaagccaattatgtgagcgtactttgggaaccacatt	872
Db	48024	AICTAAATACCAAGGCAGTATCCTTIGCTCTCTCTTCAAAAAGCTT	47977
RESULT 7			
XLCKIIB			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
COMMENT			
FEATURES			
SOURCE			
CDS			
<p>1..648</p> <p>/organism="Xenopus laevis"</p> <p>/db_xref="taxon:8355"</p> <p>/dev_stage="stage VI oocyte"</p> <p>/tissue_type="ovary"</p> <p>/cell_type="oocyte"</p> <p>/clone_lib="lambda gt10"</p> <p>1..648</p> <p>/codon_start=1</p> <p>/product="Beta subunit of casein kinase II"</p> <p>/protein_id="CAA44239.1"</p> <p>/db_xref="GI:64630"</p> <p>/db_xref="SWISS-PROT:P28021"</p> <p>/translation="MSSSEVSWISWFCGLRGNEFFCEVDYIQDFNLTGLNELEHYRALQWILDLEDELEPNQSDLEQAAEMLYGLIHARYILTNRGLAQMLEQGDGFCYPMVCEENQPMPLTGLSDIPGEAMVKLYCPKCMQVYTPKSRHHHTDGA</p> <p>TGTFPHVHPHETPRPQANQFPRLYGFKIHPMAYOLQQAASNPKSPVKTHR</p>			
BASE COUNT	185 a	142 c	149 g
ORIGIN			172 t

[illegible]

REFERENCE 1 (bases 1 to 1645)
AUTHORS Vera, M.I., Kausel, G., Barrera, R., Leal, S., Figueroa, J. and Quezada, C.
TITLE Seasonal adaptation modulates the expression of the protein kinase CK2 b subunit gene in the carp
JOURNAL Biochem. Biophys. Res. Commun. (2000) In press
REFERENCE 2 (bases 1 to 1645)
AUTHORS Vera, M.I., Kausel, G. and Barrera, R.
TITLE Direct Submission
JOURNAL Submitted (04-MAR-1999) Instituto de Biología, Universidad Austral de Chile, Casilla 567, Valdivia, Decima Region 00000, Chile
FEATURES
Source
1..1645
/organism="Cyprinus carpio"
/db_xref="taxon:7962"
1..1645
/issue_type="liver"
34..1681
/gene="CK2-b"
/gene="CK2-b"
/codon_start=1
/product="CK2 beta subunit"
/protein_id="AAF66446.1"
/db_xref="GI:7672553"
/translation="MSSSEVSWISWFCGLRGNEFFCDEVDYIQDKFNLTGLNHOVP HYKRALDMLDLEPDELEPNQSDLEFOAEMLYGLIHARYLTNRGIAQMLPKYQ QGDFGCPVRYCENQPMPLTGLSDIPGEMVLYCPKCMVDVTPKSRHHHTGATFG TGFPHLFWHPYRPRRPAQFVPRVYGFKLHPAYQCLQAASFKSPVKATR"
BASE COUNT 447 a 351 c 371 g 476 t
RIGIN

Query Match 18.3%; Score 198; DB 4; Length 1645;
Best Local Similarity 58.8%; Pred. No. 5.3e-39;
Matches 342; Conservative 0; Mismatches 240; Indels 0; Gaps 0;

397 gatgatacgtcgtggtatctctgttggtaatttgagagggaattatctctctgaa 456
|||||
46 GAGGAAGTCTGGTGAATCTTGGTCTTGGTCTACGGGAGACGATCTCTCGGAG 105
|||||
457 qtcgatgaagattattcaagatgattatcaattcttggtaatttgaagatctct 516
|||||
106 GATGAGAGACTACATCAGGACAAATCAATCTTACGGGACTCAATGAGGAATCC 165
|||||
517 taatgattatgcaattgaattcaattatagatgattgaattcccaaatgagatt 576
|||||
166 CATTACAGACAGCCCTGGACATGCTGGGATCTGGGACCTGATGAGGAGCTGGAGGAC 225
|||||
577 actgatgaacagcatgaaatgtgggaatcagctgtcagatgctatattctattcat 636
|||||
225 AACCTAACCGAGTACCTGATGAGGAGGCTGCTGAGATGCTGTATGAGCTGATCCAT 285
|||||
637 gtlcqttaacattttagactactaaagaagaatggctgcaatgaactgagaagaactgt 696
|||||
286 GCGCGCTACATCTCTACTAACCTGCGCATTCGCCAGATGCTGAGAGAGTACCAGCAGGGA 345
|||||
697 gatttcgggagagagcagagagtttcttcttggcgttcaattctgtctccas; lgaacaa 756
|||||
346 GNTTTTGGCTATTGCTCTCTGTTTACTGTGAGAAATCAGCAATGCTGCCATTGGCGCTC 405
|||||
757 tccgatatcccgagatgagactgtgaagatactatctgctcaaatgcgaggaatatct 816
|||||
406 TGTGACATCTCTGGCGAGGCGCATGGTGAGCTTACTGCGCTTAAGTGTATGATGTGATC 465
|||||
817 taacccgcatctaaattccaaggaatatttgatggagcgtactttgaaaccacattctct 876
|||||
466 ACACCCAAAGTCCTCAGGCCACCATCACCGATGAGCGCTATTTTGGCACTGCTTTCCCC 525
|||||
877 caattgtcttggacttaacggaacttaaacccgcagagaagctactcaaaagctatgac 936
|||||
526 CAGATGCTCTTCAATGAGTGCATCTGATACCGGCCAAAGAGGCCCTGCAACACCAAGTTTGTG 585
|||||
937 ccaaaaattcttggcttcaaggttacacaacaaccatgatactag 978

Db 586 CCACGGCTCTATGTTTCACGATTCACCAAGGCTTACCAG 627
|||||
RESULT 1C
LOCUS MMCK11B 914 bp mRNA ROD 12-SEP-1993
DEFINITION Mouse mRNA for casein kinase II beta subunit (EC 2.7.1.37).
ACCESSION X52959
VERSION X52959.1 GI:50418
KEYWORDS casein kinase; protein kinase.
SOURCE mouse
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 914)
AUTHORS Canaani, D.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-1990) Canaani D., Tel Aviv University, Department of Biochemistry, Tel Aviv University, Tel Aviv 69978, Israel
REFERENCE 2 (bases 1 to 914)
AUTHORS Kopatz, I., Naiman, T., Eli, D. and Canaani, D.
TITLE The nucleotide sequence of the mouse cDNA encoding the beta subunit of casein kinase II
JOURNAL Nucleic Acids Res. 18 (12), 3639 (1990)
COMMENT Data kindly reviewed (27-AUG-1993) by Canaani D.
FEATURES
Source
1..914
/organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/dev_stage="pre B"
/cell_line="702/3"
/clone_lib="lambda g11"
128..775
/note="casein kinase II beta subunit (AA 1-215)";
/codon_start=1
/protein_id="CAA37132.1"
/db_xref="GI:50419"
/db_xref="MGD:MGI:88548"
/db_xref="SWISS-PROT:P13862"
/translation="MSSSEVSWISWFCGLRGNEFFCDEVDYIQDKFNLTGLNHOVP HYKRALDMLDLEPDELEPNQSDLEFOAEMLYGLIHARYLTNRGIAQMLPKYQ QGDFGCPVRYCENQPMPLTGLSDIPGEMVLYCPKCMVDVTPKSRHHHTGATFG TGFPHLFWHPYRPRRPAQFVPRVYGFKLHPAYQCLQAASFKSPVKATR"
BASE COUNT 215 a 268 c 214 g 217 t
ORIGIN

Query Match 16.9%; Score 183; DB 12; Length 914;
Best Local Similarity 57.7%; Pred. No. 2.9e-35;
Matches 327; Conservative 0; Mismatches 240; Indels 0; Gaps 0;

QY 396 tgaatgacgtcgtggtatctctgttggtaatttgagagggaattatctctctgaa 455
|||||
Db 139 TGAGGAGGTGCTCGAATTCCTGCTGTTGGGCTCCGTGGTAATGATCTCTCTGGA 198
|||||
QY 456 aglcgaagaagattatcaagatgatttcaaatcttctgtggttaagtgtcaagtccc 515
|||||
Db 199 GCTGGATGAAGACTACATCCAGGACAAATTTAATCTTACTGGACTCAATGAGCAGGTGCC 258
|||||
QY 516 ttaactatgattatgcaattgactctattttagatgattgattcttcccaagtgagatt 575
|||||
Db 259 TCACATATGACAAAGCTCTGGACATGATCTTAGACCTGGAACCTGATGAAGAGCTGGAAGA 318
|||||
QY 576 tactgatgaacagcatgaaatggtggaatcagctgctgctgagatgctatgcttattca 635
|||||
Db 319 CAACCCCAACAGCAGGACTTGATGACAGGACGCTGAGATGCTTTATGGTTGATCCCA 378
|||||
QY 636 tggctgtacattttgactartaaaggaatggctgcaatgactgagaagtacaagaactg 695
|||||
Db 379 CCGCGGCTACATCCTCACCACCGAGGCGATCGCACAAATGTTGGAAAGTACCAGCAGGG 438
|||||

636	tgatttcggagatgcccgagaaattttctgttggcgcgaatttctgcttcagttgaca	755
637		
638		
639	AGACTTGGCTACTGCTCCTGTATACTGTGAGAACACAGSCAATGCT CCTATCGGCC	495
640		
641		
642		
643		
644		
645		
646		
647		
648		
649		
650		
651		
652		
653		
654		
655		
656		
657		
658		
659		
660		
661		
662		
663		
664		
665		
666		
667		
668		
669		
670		
671		
672		
673		
674		
675		
676		
677		
678		
679		
680		
681		
682		
683		
684		
685		
686		
687		
688		
689		
690		
691		
692		
693		
694		
695		
696		
697		
698		
699		
700		
701		
702		
703		
704		
705		
706		
707		
708		
709		
710		
711		
712		
713		
714		
715		
716		
717		
718		
719		
720		
721		
722		
723		
724		
725		
726		
727		
728		
729		
730		
731		
732		
733		
734		
735		
736		
737		
738		
739		
740		
741		
742		
743		
744		
745		
746		
747		
748		
749		
750		
751		
752		
753		
754		
755		
756		
757		
758		
759		
760		
761		
762		
763		
764		
765		
766		
767		
768		
769		
770		
771		
772		
773		
774		
775		
776		
777		
778		
779		

Cy		396	tgatgataacgcggatcttcgttatttgtaattttagaggagaagtattctcttgtga	458
Df		133	TGAGGAAGCTTCCTCGATTTCCCTGGTTCCTGTGGCCTGCCGTGTAATAAATCTCTGTGA	192
Cy		456	aactcgatgaagattatatcaaatgaattccaattttcgaatttbtgtttaagtggtcaaaccc	515
Df		193	GTTGGTGAGAGACTACATCAAGGCACAATTAACTTACTTGACTCAATAGACGAGTCCC	252
Cy		516	ttactatgatttagcacttgatctcatcttatagatttgattgtgtcccaccagtgagtgtt	575
Df		253	ICACTAACGAAGAAGCTCTGGACATGATCTTAGACCCTGGAAACCTGATGAAGAGCTGGAAGA	312
Cy		576	tactgataaacagcatgaatagtggaatcacgclartsgadatgatalatgcttattcca	635
Df		313	CACCCCCAACGACGAGCATGTGATCGAACAGGCAGCTGAGATGCTTTATGGCTTGAACCA	372
Cy		636	tgttggttacattttgactactaaaagaatggctgcgaatgactgagaagtaacaagaactg	695
Df		373	CGCCCGGTACATCTTCACCAACCGAGGCATCGCACAAATGTTGGAAAAATACCACGACGG	432
Cy		696	tgattttggagagagccccagaggtttctgtllygcgtcagttttgtctccagttcgga	755
Df		433	AGACTTTGGCTACGTGCTCTGTGTATCTGTGTGAAGACCGACCAATGCTTCCATCGGCT	492
Cy		756	atscgatataccgagatcgagttactgtgaagatatactacctcttaaagcgagatatact	815
Df		493	ITCAGACATCCGAGCGACGCCAATGGTGAACCTCIACTGCCCAAAGTGATGGACCTGTGA	552
Cy		816	ttaccgcgcatataattccaggccaatttgatggagctactttggaaaccacattccc	875
Df		553	CAGACCCAAGTCTCCAGACACCCACACAGCGAGCGGCATACTTTGGCACTGTGTTCGC	612
Cy		876	tcactgttcttgatgacttacgggaacttaaaagccgacgaagccctactcaaaagctatg	935
Df		613	TCACAIGCTCTTCATGTGTGATCCAGATPACCGCCGCCAAGCGACCTGCCCAACCGATTGT	672
Cy		936	cccaaataatctllggttccaggtaca	962
Df		673	ACCCAGGCTCTATGGTTTCAAGATCCA	699

RESULT 12
HCKII

LOCUS	HCKII	921 bp	mRNA	PRI	12-SEP-1993
DEFINITION	Human mRNA for phosphoinositide kinase II beta subunit.				
ACCESSION	X16312				
VERSION	X16312.1	GI:29964			
KEYWORDS	casein kinase II; phosphotin.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;				
AUTHORS	Primates; Catarrhini; Hominoidea; Homo.				
TITLE	Jakobi,R., Voss,H. and Pyerin,W. Human phosphoinositide kinase type II. Molecular cloning and sequencing of full-length cDNA encoding subunit beta				
JOURNAL	Eur. J. Biochem. 183 (1), 227-233 (1989)				
MEDIA LINE	8325346				
COMMENT	Data kindly reviewed (26-OCT-1989) by Jacobi R.				
FEATURES	Location/Qualifiers				
source	1..921				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	/cell_line="HeLa S3"				
	/clone_lib="lambda gt10"				
	134..781				
	/note="phosphitin/casein kinase II beta subunit: (AA 1-				
	134..781				
	/protein_id="CAA34379.1"				
	/db_xref="GI:29964"				
	/translation="MSSSEVSNWFCGRNEFFVEVDYIQDKNLNLTGLIHYEQALMDLPEDELDENPNQSLIEQAAMELYGHARYILTNRGIQM				

CDS

QGFYCYPRVYCNQPMPLIGLSIDPGFAMVKLYCPKMDVYTPKSSRHHHTTGAVFG
TGFPHMLFEMVHPYRPRKPNQFVPRLYGKFIHPMAYQLQLOAASNFKSPVKIIR

misc_feature 901..906
/note="pot. polyA signal"

polyA_site 921
/note="polyA site"

SE COUNT 211 a 274 c 217 g 219 t
IGIN

Query Match: 16.9%; Score 182; DB 66; Length 921;

Best Local Similarity 56.5%; Pred. No. 5.1e-35;

Matches 338; Conservative 0; Mismatches 260; Indels 0; Gaps 0;

365 gtgaagggtcgaatgagtgagtcggagtgatgatacattggtatctctgtttt 424

114 CHCCAGCCGTCACCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 173

425 gtaatttgagaggggaatgattttcttctggaagtcgaatgataatgaaatgall 484

174 GTGGGCTCCGTGGCAATGAATCTTCTGTGAAGTGGATGAAGTGAAGTGAAGT 233

485 taaattcttggttttaagtgatgaagtcatttactgattgattgattgatttct 544

234 TTAATCTTACGGACTCAATGACGAGGTGCTCTACATGCAACACTCTAGACATGAT 293

545 taatggttgatgcttcccaagtcgagtgatgatttactgatacaatgataatgaggaat 604

294 TGACCTTGAGCTGATGATGAAGTGGAGGACACCCCAACAGAGTGAAGTGAAGT 353

605 caattgctgaagatgattatgatttcttctggaagtcgaatgataatgaaatgall 664

354 AGGCAGCGGAGATGCTTATGCAATGATCAGCGCGGCTACATCTTACAGCGGTGCA 413

665 tggctggaatgactgagagtgataagagtcgtgatttcggagagtcgagagtttct 724

414 TCGCCCAAGATGTTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 473

725 gtgcggtcagtccttcttcagttgagaaatgagatccgagagtcgagagtcgag 784

474 GTGAGAACCGCAATGCTTCCATTCGCTTTCAGACAACCCAGTGAAGCCATGCTGA 533

785 aqatataatgactaaatgagagtgataatcttaccgagtcgataatcttaccaggaat 844

534 AGCTCTACITGCCCCAAGTGGATGATGATGATGATGATGATGATGATGATGATGAT 593

845 ttgagtgagtcgactttggaacacacattctctctctctctctctctctctctct 904

594 CGGATGGGCGCTTACTTCGGCACTGGTTCCTTCAGATCTCTTCAIGTGCATCCCGAGT 653

905 taaagccgagagtcactctcaagtcgagtcgagtcgagtcgagtcgagtcgagtcgag 962

654 ACCGCCCAAGAGACTGCCCCACCAAGTTCGTCGCCAGGCTCTACGGTTTCAGATCCA 711

SCUL 13

CUS

FINITION

HSCKIFB

921 bp

mRNA

PRI

12-SEP-1993

Human mRNA for phosphatase type II beta subunit (EC

2.7.1.37).

CESSION

X16937

RSION

YWORDS

URCE

ORGANISM

Human sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;

Primates; Catarrhini; Hominoidea; Homo.

Jakobi, R., Voss, H., and Peyer, W.

Human phosphatase/casein kinase type II. Molecular cloning and

sequencing of full-length cDNA encoding subunit beta

Eur. J. Biochem. 183 (1), 227-233 (1989)

89325340

MEDLINE

FEATURES
source

Location/Qualifiers
1..921
/organism="Homo sapiens"

/db_xref="taxon:9606"

/tissue_type="epithelium"

/cell_line="Hela S3"

/clone_lib="lambda gt10"

/clone="CKII-beta"

134..781

/note="phosphatase/casein kinase type II beta subunit (AA 1

- 215)"

/protein_id="C343481.1"

/db_xref="GI:29967"

/db_xref="SWISS-PROT:P13862"

/translation="MSSSEVSWISWFCGLRGNRFFCEVDEYIQDKPMLTGLNKPVP

HYKADLMILDEPDEEDNPNQSLIQAAEMLYGLIHARYIITNKGIAQMLEKYQ

QSDFGYCPVYCNQPMPLIGLSIDPGFAMVKLYCPKMDVYTPKSSRHHHTDGAVFG

TGFPHMLFEMVHPYRPRKPNQFVPRLYGKFIHPMAYQLQLOAASNFKSPVKIIR"

misc_feature 901..906

/note="pot. polyA signal"

polyA_site 921

/note="polyA site"

BASE COUNT 211 a 274 c 217 g 219 t

ORIGIN

Query Match 16.9%; Score 182; DB 66; Length 921;

Best Local Similarity 56.5%; Pred. No. 5.1e-35;

Matches 338; Conservative 0; Mismatches 260; Indels 0; Gaps 0;

QY 365 gtgaagggtcgaatgagtgagtcggagtgatgatacattggtatctctgtttt 424

DB 114 CHCCAGCCGTCACCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 173

QY 425 gtaatttgagaggggaatgattttcttctggaagtcgaatgataatgaaatgall 484

DB 174 GTGGGCTCCGTGGCAATGAATCTTCTGTGAAGTGGATGAAGTGAAGTGAAGT 233

QY 485 taaattcttggttttaagtgatgaagtcatttactgattgattgattgatttct 544

DB 234 TTAATCTTACGGACTCAATGACGAGGTGCTCTACATGCAACACTCTAGACATGAT 293

QY 545 taatggttgatgcttcccaagtcgagtgatgatttactgatacaatgataatgaggaat 604

DB 294 TGGACCTTGAGCTGATGATGAAGTGGAGGACACCCCAACAGAGTGAAGTGAAGT 353

QY 605 caattgctgaagatgattatgatttcttctggaagtcgaatgataatgaaatgall 664

DB 354 AGGCAGCGGAGATGCTTATGCAATGATCAGCGCGGCTACATCTTACAGCGGTGCA 413

QY 665 tggctggaatgactgagagtgataagagtcgtgatttcggagagtcgagagtttct 724

DB 414 TCGCCCAAGATGTTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 473

QY 725 gtgcggtcagtccttcttcagttgagaaatgagatccgagagtcgagagtcgag 784

DB 474 GTGAGAACCGCAATGCTTCCATTCGCTTTCAGACAACCCAGTGAAGCCATGCTGA 533

QY 785 aqatataatgactaaatgagagtgataatcttaccgagtcgataatcttaccaggaat 844

DB 534 AGCTCTACITGCCCCAAGTGGATGATGATGATGATGATGATGATGATGATGATGAT 593

QY 845 ttgagtgagtcgactttggaacacacattctctctctctctctctctctctctct 904

DB 594 CGGATGGGCGCTTACTTCGGCACTGGTTCCTTCAGATCTCTTCAIGTGCATCCCGAGT 653

QY 905 taaagccgagagtcactctcaagtcgagtcgagtcgagtcgagtcgagtcgagtcgag 962

DB 654 ACCGCCCAAGAGACTGCCCCACCAAGTTCGTCGCCAGGCTCTACGGTTTCAGATCCA 711

RESULT 14

```

CKLB
CUS      SPCK118      837 bp      mRNA      PLX      27-JAN-1994
FINITION  S.pombe mRNA for casein kinase II beta subunit.
CESSION   X74274
VERSION   X74274.1 GI:452289
WORDS     casein kinase II; casein kinase II beta subunit.
ORIGIN    fission yeast.
ORGANISM  Schizosaccharomyces pombe
          Eukaryota; Fungi; Ascomycota; Ascomycetes;
          Schizosaccharomycetales; Schizosaccharomycetaceae;
          Schizosaccharomycetes.
          1 (bases 1 to 837)
          Direct Submission
          Submitted (21-JUL-1993) I. Roussou, EMBL, Differentiation
          Programme, Meyerhofstrasse 1, 69117 Heidelberg, FRG
          2 (bases 1 to 837)
          Roussou, I. and Prætorius, G.
          The Schizosaccharomyces pombe casein kinase II alpha and beta
          subunits: evolutionary conservation and positive role of the beta
          subunit
          Mol. Cell. Biol. 14 (1), 576-586 (1994)
          94088557
          Location/Qualifiers
            1..837
            /organism="Schizosaccharomyces pombe"
            /strain="wild-type"
            /db_xref="taxon:4896"
            /clone_lib="ZAP11 S.pombe cDNA"
            61..756
            /gene="ckb1"
            61..756
            /gene="CKB1"
            /codon_start=1
            /product="casein kinase II beta subunit"
            /protein_id="CAA52330.1"
            /db_xref="GI:452290"
            /translation="MQLYSSESDSDQYVVDHFLG:KGNFECEVDEDFIDRENLT
            GLSHEVPHYSQSLDILVDLPDLPPEVQDEVEASRHLXGLHARYILTACGLYKML
            EYKKCPDGHCPVLNCQPMPLVGLSDIAHAKSVKLYCPCECDVYTPKSKRIASIDG
            AYFQTSFPHMI:FOYPELAVPKSFYRIPRIFPKVHSYSAIPKQDQVYKEXKKRIQ
            CAEAFSKNLAIT"
          SE COUNT      261 a 165 c 161 g 250 t
         IGIN

Query Match      16.8%; Score 161.4; DB 34; Length 837;
Best Local Similarity 58.8%; Pred. No. 7,20-35;
Matches 336; Conservative 0; Mismatches 226; Indels 9; Gaps 1;

394 gctatgatcacatcgaggatccttggcttttgaatttgaaggaagatctctctgt 453
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
91 GATGATCTCAATATTCGCTGATCGTTT:TAGCAGTAAAGGAAGCAATTTTTCG 150
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
454 gaatgatgaagatataattcaagatgatttcaatcttggtttgaatggatcaagtc 513
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
151 GAAGTCGAGAGAGACTTCACGAGTACGCTTAAATTTGACTGGATTGATGATCAAGTT 210
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
514 ccttactatgatgatgcattgatctcattcattgatgttggatgttcccaagtgatg 573
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
211 CCACAGTACCCAGTCGCTTACAGCCCATTTTATGATG:ATTGGATCCGCA----- 261
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
574 ttctatgatgaacagcatgaatqgttggagatcagctgctatataatctcttatt 633
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
262 TTACACAGAGAG:ACAAGATGAGGTAGAGGACTGCTCCCTCATTTGTACGGCTTAT 321
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
634 catgttgcatttactactaagaagaatgggtgcgaatgactgagaagtaagaagac 693
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
322 CAGCGCGGTATATCTTAAGGCTCAGGCTTATATAAATGCTTGAGAAATACAAAAA 381
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
694 tggatttcggagagacccgagaggtttctcttgcgttcagctcttctcccaattgga 753
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```



```

396 tgaatgaacgtcgggagatctcttggttttgaatttgaggaggaatgattctctctgtga 455
125 TGAGGAGGTGTCTGGATTTCCTGCTGGGCTCGGTGTAATGATGATGCTTCTGTGA 184
456 agtcgatgaagatattatcaagatgatttcaatcttctgtggttlaagtgatcaagtc 515
185 GGTGGATCAAGACTACATCCAGGACAAATTAATCTACTGGACTCAATGAGCAGGTGCC 244
516 ttactatgattatgcacttgatctcattttatagatgttgaatctcttccaaacactgaagatgtt 575
245 TCATATGCGAAGAGCCCTAGACATGATCTTGGAGCTGGAACTGATGANGAGCTGGGAAGA 304
576 tactgatgaacagcatgaaatggttggaaatcagctgctgagatgctatattgtcttattcca 635
305 CAAACCCCAACCCAGAGAGTGNCTTGAATGAGCAGGCGCGGAGATGCTCTATGGGTGATCCA 364
636 tgttcattacatttgaactactaaagaatgagctggcaatgactgagaaatcaagaactg 695
365 GCGCCGCTACATCTCTACCAACCGGGGCAATGGACAAAATGTTGGAAGATACCAAGG 424
696 tgatttcgggagatgcccgagagtttctgttgggtcagtccttcttccagttgaca 755
425 AGACTTTGGCTACTGTCTCTCGAGTATCTGTGAGAACGACGCGGATGCTTCCCATCGGCT 484
756 atccgatatcccgagatcgagctactgtgaagatatacttgcctaaatggaggagatatc 815
485 TTGGACATCCAGGAGGAGGCGCATGGTGAAGCTCTACTGGCCCAAGTGCATGGAGCTGTA 544
816 ttaccgagatctlaaatccaaagcaatattatgagagcgtactttggnaaccacatccc 875
545 CACACCCCAAGTCCCTTAGGCAACCAACAGCATGGGCGCATACTCGGCAATGGTTTCCC 604
876 tcaattgttctgtatgaactttacaggaactttaaagccgacaaagcctactcgaagctatgt 935
605 TCATATGCTCTCATGGTGCATCCGGAGTACCGGCGGAGCGGCGGCGGCGGCGGCGGCGG 664
936 cccaaaaatctttggcttcagggtaca 962
665 GCGGAGGCTCTACGGTTCAGAGATCCA 692

```

```

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

nucleic - nucleic search, using sw model
n on:      November 15, 2000, 11:23:05 : Search time 749.05 Seconds
              (without alignments)
              8914.533 Million cell updates/sec

tlo:      us-09-359-026-1
rfect score: 1080
quence:    1 gtcgacccacgcgtccgaga.....tggagcaccatcaaccatt 1080

oring table: IDENTITY_NUC
              Gapop 10.0 , Gapext 1.0

arched:     7189864 seqs, 3091403243 residues

tal number o: hits satisfying chosen parameters:      14375728

qiumum DB seq length: 6
ximim DB seq length: 2000000000

st-processing: Minimum Match 6%
               Maximum Match 100%
               Listing first 45 summaries

tabase :
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
12: gb_est12:*
13: gb_est13:*
14: gb_est14:*
15: gb_est15:*
16: gb_est16:*
17: gb_est17:*
18: gb_est18:*
19: gb_est19:*
20: gb_est20:*
21: gb_est21:*
22: gb_est22:*
23: gb_est23:*
24: gb_est24:*
25: gb_est25:*
26: gb_est26:*
27: gb_est27:*
28: gb_est28:*
29: gb_est29:*
30: gb_est30:*
31: gb_est31:*
32: gb_est32:*
33: gb_est33:*
34: gb_est34:*
35: gb_est35:*
36: gb_est36:*
37: gb_est37:*
38: gb_est38:*
39: gb_est39:*
40: gb_est40:*
41: em_estba:*
42: em_estfun:*
43: em_esthum1:*
44: em_esthum2:*
45: em_esthum3:*
46: em_esthum4:*
47: em_esthum5:*
48: em_esthum6:*
49: em_esthum7:*
50: em_esthum8:*
51: em_esthum9:*
52: em_esthum10:*
53: em_esthum11:*
54: em_esthum12:*
55: em_esthum13:*
56: em_esthum14:*
57: em_esthum15:*
58: em_esthum16:*
59: em_esthum17:*
60: em_esthum18:*
61: em_esthum19:*
62: em_esthum20:*
63: em_estin1:*
64: em_estin2:*
65: em_estin3:*
66: em_estin4:*
67: em_estom:*
68: em_estov1:*
69: em_estov2:*
70: em_estpl1:*
71: em_estpl2:*
72: em_estpl3:*
73: em_estpl4:*
74: em_estpl5:*
75: em_estrol:*
76: em_estro2:*
77: em_estro3:*
78: em_estro4:*
79: em_estro5:*
80: em_estro6:*
81: em_estro7:*
82: em_estro8:*
83: em_estro9:*
84: em_estrol10:*
85: em_estrol11:*
86: em_estrol12:*
87: em_estrol13:*
88: gb_gss1:*
89: gb_gss2:*
90: gb_gss3:*
91: gb_gss4:*
92: em_gss1:*
93: em_gss2:*
94: em_gss3:*
95: em_gss4:*
96: gb_gss5:*
97: gb_gss6:*
98: gb_gss7:*
99: gb_gss8:*
100: gb_gss9:*
101: gb_gss10:*
102: gb_gss11:*
103: gb_gss12:*
104: gb_gss13:*
105: gb_gss14:*
106: gb_gss15:*
107: gb_gss16:*
108: gb_gss17:*
109: gb_gss18:*
110: gb_gss19:*
111: gb_gss20:*
112: gb_gss21:*
113: gb_gss22:*
114: gb_gss23:*
115: gb_gss24:*
116: em_gss5:*
```

117: em_gss6:*
 118: em_gss7:*
 119: em_gss8:*
 120: em_gss9:*
 121: em_gss10:*
 122: em_gss11:*
 123: em_gss12:*
 124: em_gss13:*
 125: em_gss14:*
 126: em_gss15:*
 127: em_gss16:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY:

Result No.	Score	Query Match	Length	DB ID	Description
1	473.2	43.8	499	14	AT993201
2	431	39.9	431	19	AV551311
3	426.8	39.5	544	29	T42848
4	359.5	33.3	642	13	A1881573
5	340.4	31.5	412	39	T42705
6	334	30.9	603	14	AT996697
7	331.8	30.7	803	21	AW350255
8	326.6	30.4	477	39	T45989
9	321.4	29.8	366	39	T45841
10	303	28.1	496	21	AW277268
11	290.5	26.9	655	22	AW433059
12	286.8	26.6	543	24	AW777192
13	279	25.8	562	35	BF40549
14	269.2	24.9	634	13	A1501529
15	250	23.2	566	23	AW671986
16	249.8	23.1	478	22	AW508109
17	243.8	22.6	249	40	Z34116
18	240	22.2	610	12	AT1746013
19	239.4	22.2	583	36	BF492453
20	234.4	21.7	570	35	BF474548
21	234.2	21.7	505	19	AV538974
22	232	21.5	645	15	A0030812
23	230.2	21.3	501	21	AW286827
24	224.2	20.8	715	34	BE319805
25	222.2	20.6	626	21	AW307470
26	217.8	20.2	562	25	AW982908
27	212.6	19.7	653	14	AT1947676
28	210.6	19.5	595	21	AW309638
29	201.8	18.7	567	35	BE440281
30	201	18.6	949	24	AW726948
31	195.6	18.1	430	33	BE058831
32	192.8	17.9	539	24	AW747488
33	192.4	17.7	585	7	AA979779
34	191	17.7	601	10	A1477862
35	189.4	17.5	351	35	BE460243
36	187.8	17.4	549	10	A1415745
37	186.5	17.3	447	37	H37389
38	183.6	17.0	641	34	BF302855
39	180.4	16.7	465	24	AW760221
40	168.2	16.7	856	34	BE194657
41	179	16.6	553	32	BE015871
42	179	16.6	654	25	AW914248
43	177.2	16.4	619	12	AT1726332
44	176.6	16.4	891	9	AT323164
45	174.4	16.1	621	8	AT109297

ALIGNMENTS

LOCUS AI993201 499 bp mRNA EST C8-SEP-1999
 DEFINITION CDNA clone 701495685, mRNA sequence.
 ACCESSION AI993201
 VERSION AI993201.1 GI:5840106
 KEYWORDS ESI.
 SOURCE Arabidopsis thaliana
 ORGANISM Arabidopsis thaliana
 thale cress.
 REFERENCE 1 (bases 1 to 499)
 AUTHORS Chen, J., Momiyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D., Wang, X., Hillman, J., Guebler, K., Kim, C., Doyle, M., Brzoska, P., Gordone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D., Tan, R., Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T., Pollock, J., Suzuki, G., Argenciere, C., Shah, S., Nobrila, A., Murry, L., Turner, C., Sukorian, S., Eider, L. and Hanson, D.
 Arabidopsis thaliana Gene Expression MicroArray
 Jpublished (1999)
 CONTACT: David Smoller, Ph.D.
 Genome Systems, Inc., a wholly owned subsidiary of Incyte
 Pharmaceuticals, Inc.
 4633 World Parkway Circle, St. Louis, MO 63134, USA
 Tel: 877-577-2733
 Fax: 314-427-3324
 Email: service@genomesystems.com.
 FEATURES
 Location/Qualifiers
 1..499
 /organism="Arabidopsis thaliana"
 /db_xref="taxon:3702"
 /clone="701495685"
 /clone_lib="A. thaliana, Ohio State clone set"
 /note="cDNA library was made from selected clones from the Arabidopsis thaliana Ohio State clone set."
 BASE COUNT 141 a 82 c 120 g 155 t
 ORIGIN
 Query Match 43.8% Score 473.2 DB 14 Length 499;
 Best Local Similarity 98.2% Pred. No. 5.9e-122;
 Matches 489; Conservative 0; Mismatches 8; Indels 1; Gaps 1;
 QY 110 attcttgccttttttgagaagaaatcgaattatgtacaaggaaactagtg-gaggaggt 168
 |||||
 DB 1 ATTTCTGTCTTTTGGAGAGGAATCGAAATATGTACACGAACTAGTGATAGGAGGT 60
 |||||
 QY 169 ggtggggggtcgcgacgacgagatcccggtgggagctattgacggaacgaatcaac 228
 |||||
 DB 61 GG*GGTGGGTGATCGAGATCGAGATCCTCGGTGGAGCTATTGATCGAAACCAATCAAC 120
 |||||
 QY 229 gatgcactcaataagaactagagaattttcaacttcaaccacacatcagggttttc 288
 |||||
 DB 121 GATGCACTCAATAAGAAACTAGAGAAATCTTCAACTTCCACCACCATAGGGTTTC 180
 |||||
 QY 289 tcttcaaaacaaagatcccttttcttcacatctacaaactcagcttctcgtggtg 348
 |||||
 DB 181 TCCTCTTAACACAAAGATCCCTTTTCTCTCACATCTACTAAAACIAGCTTCTGTATGTC 240
 |||||
 QY 349 qaalcggaaactgatagtggaaggtctggtgagtgagtgagtgagtgagtgagtgagtgag 408
 |||||
 DB 241 GAATCGAAACIATAGTAGAGGTCTGTATGTAGTGGATCGAGGGGTGATGATACGTCG 300
 |||||
 QY 409 tggatctcttgggttttgtaatttgagaggaatgattcttctgtgaagtcatgaagt 468
 |||||
 DB 301 TGGATCTCTGGTTTTGTAAATTSAGAGGAATGATTTCTCTGGAAGTCGATGAAGAT 360
 |||||
 QY 469 tatallcaagatgatttcaatttttgggttaagtggtggtggtggtggtggtggtggtggtggt 528
 |||||
 DB 361 TATATTCAGATGATTTCATCTTTTGGGTTPAAGTGGTCAAGTCCCTTACTATGATTAT 420
 |||||
 QY 529 qcacttgatctatctttagatgttgatgtcttccacacagtgagatggttactgatgaacag 588
 |||||

428 attgagaggaatgatttcttctgtgaagtcgagatgattatcaagatgattcca 487
 121 ATTGAGAGGGAATGATTCTCTGCGTGAAGTCGATGAAGATTATATCAAGATGATTC 180
 486 attctctctgtgttaagtgatcaagtccttactatcaatgactgactgacttact 547
 181 ATCTTCTGTGTTAAGTTCCTCAAGTCTCTACTATGATGATATPNCACATTCAGTCAITTAG 240
 548 algttgatgtcttcaacagtgagatgttactatgaacacatgaagatgagatgagacag 607
 241 ATGTTGATGCTTCCACAGTGAGATGTTTACTGATGAACAGCATGAATGTTGGATATCAG 300
 608 ctgtgagatgctatagtggtcttattcatgttcttctca-ttttgactactana-aggaa 564
 301 CTGTGAGATGCTATAGTGTCTTATCAATGTTCTGTACATTTTGTACTACTAANAGGAA 360
 565 tggctgaatgactgagaagatacaagacagtg-attctgagagagagagagagagall 721
 361 TGGCTGGAATGACTNAGNAGTCAAGAAAGCTGTGNATTCGGGAGATCGGGTACTT 420
 722 tctgttgcgtcactctctcttccagltggaacatccgatatcccgagatcagactag 782
 421 TCNTTCGGGNCAGCCTTGCTTCCAGTGGNKAACCGATATCCGAGATCGGGTACTT 480
 782 tgaagacatactgcccataatgagagatatcttaccggagatcaaatc 834
 481 TGAAGGATATACGCGCC-AAATCNGGGGTATNTCTTNCNGNCGTAAATCC 532

SUFF 4

A1881573 612 bp mRNA EST C2-FEB-2000
 606070H09.V1 606 - Ear tissue cDNA library from Schmidt lab Zea
 mays cDNA, mRNA sequence.
 A1881573
 A1881573.1 GI:5555622
 EST.
 Zea mays.
 Zea mays.
 Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
 Walbot,V.
 Maize ESTs from various cDNA libraries sequenced at Stanford
 University
 Unpublished (1999)
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 606070 row: H column: 09.
 Location/Qualifiers
 1. 612
 /organism="Zea mays"
 /cultivar="Oti043"
 /db_xref="taxon:4577"
 /clone_lib="606 - Ear tissue cDNA library from Schmidt
 lab"

FEATURES
 source
 1. 612
 /organism="Zea mays"
 /cultivar="Oti043"
 /db_xref="taxon:4577"
 /clone_lib="606 - Ear tissue cDNA library from Schmidt
 lab"

SEQUENCE
 154 c 147 c 148 g 163 t
 IGIN

Query Match 33.3%; Score 359.6; DB 13; Length 612;
 Best Local Similarity 77.8%; Pred. No. 4.3e-90;

Matches 434; Conservative 0; Mismatches 124; Indels 0; Gaps 0;
 QY 341 ctgagtgtgaatcggaactgaagtgagaggggtctgagtgtgagatcgagggtgagt 400
 Db 55 CCGAAGGGGAGTCTGATTCTGTAGTGAAGCAATCAAGTGTAGTGGCTCTGATGGAGAAG 114
 QY 401 atagctcggtgagatctctgtgttllglaatttgagaggggaatgattctctctgtgaagtcy 460
 Db 115 ACACCTCGGTGATTTCATGATTTGCAACTTAAAGAGGAATGAGTTCCTGTGAAGTCG 174
 QY 461 atgaagatataatcaagatgatttcaatcltllgtggtttaagtgtcaagcccttact 520
 Db 175 ATGATCACTACATTCAGAGCGACTTCAAGCTTTTGGCCTCAGACCGCAAGTTCCTTAT 234
 QY 521 atgattatgacttgcactctcattttagatgltgacacctccaacagatgaatgattactc 580
 Db 235 ATGATTATGCTCTTGTATCTCATTTTAGATATTGATCATCTCAITGGTGATATGTTCACTG 294
 QY 581 atgaacagatgaaatgggtggaatcagctgctgagatgctatattgctcttattctatct 640
 Db 295 AGCAACAATAGTACGTCGGAGAAATCAGCTGCAGAGATGCTTTAIGGGCTGATCCATGCAC 354
 QY 641 gttacattttgactactaaagaaatagctgcaatgactgagaagtaacaagaactgatt 700
 Db 355 GATACATCTCTGACCACTAAAGGGCTGCCTGCAATGCTGGAGAAGIATAGGAACATATGACT 414
 QY 701 tggagagatgccgagagagtttctgtgtcggttcagctctgtcttccagltgacaalccq 760
 Db 415 TCGGGCGGTGCCCGCGTGTACTGTCTGGTCAACCATGCTCGCGGTGGCAACAICAG 474
 QY 761 atatcccgagatgagatctgtgaagatataactgacctaaatgcgaggagatatattacc 820
 Db 475 ATATTTCATCGATCTAGTACCGTGAANAATATAGTCCCGCAAGTGTGAGACATCTACTACC 534
 QY 821 cggatctaaattccaaggaatattgtgagcgctactttggaaccacattccctcact 880
 Db 535 CACGGTCCAAAGTACCAAGCAACATCGACGGCGCATATTTGGGCAACGTTCCCTCACC 594
 QY 881 lgtttgatgacttaagc 898
 Db 595 IGTCTCTGATGACATACG 612

RF501.1 5
 T42705
 LOCUS
 DEFINITION
 T42705 412 bp mRNA EST 07-JAN-1998
 5968 Lambda-PRL2 Arabidopsis thaliana cDNA clone 116C2217, mRNA
 sequence.
 T42705
 VERSION
 T42705.1 GI:2757956
 KEYWORDS
 EST.
 SOURCE
 thale cress.
 ORGANISM
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 412)
 Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh
 L., Ohlridge,J., Raikhel,N., Somerville,S., Thomashow,M., Retzel
 E. and Somerville,C.
 Genes galore: a summary of methods for accessing results from
 large-scale partial sequencing of an anonymous Arabidopsis cDNA clones
 plant physiol. 106, 1241-1255 (1994)
 95148729
 COMMENT
 On Jan 7, 1998 this sequence version replaced qi:947366.
 Contact: Thomas Newman
 MSU-DOE Plant Research Laboratory
 Michigan State University
 MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
 Lansing, MI
 Tel: 517-353-0854
 Fax: 517-353-9168
 Email: 22313tcn@lhm.cl.msu.edu

Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids 1;
Fabales; Fabaceae; Papilionoideae; Glycine.

REFERENCE AUTHORS TITLE JOURNAL COMMENT

1 (bases 1 to 903)
Vodkin, L., Keim, P., Shoemaker, R., Retzel, E., Khanna, A., Corryell, V.,
Eppelring, J., Raph, C., Shoop, E., Pardini, J., Liu, L., and Lewin, B.
A Functional Genomics Program for Soybean (NSF 9872565)
Unpublished (1999)
Contact: Vodkin, L.O., P., A Functional Genomics Program for
Soybean (NSF 9872565)
Lewin, B. A. Director, Keck Center for Comparative and Functional
Genomics
University of Illinois
Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
Tel: (217) 244-6147
Fax: (217) 333-4562
Email: l-vodkin@uiuc.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134. For further information
call: (800) 430-0030 or (314) 427-3222 FAX: (638) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or info@genome
systems.com web site: www.genomesystems.com
Seq primer: 5'-TTTTTTTCTTTTCTTTT(A/C/G)-3'
Location/Qualifiers
..803
/organism="Glycine max"
/cultivar="Williams"
/db_xref="taxon:3847"
/clone_lib="cd-1821"
/tissue_type="root"
/lab_host="X120-Gold"
/note="Vector: p Bluescript II XR; Site 1: EcoRI; Site 2:
XhoI; Library Gm-r1021 is a sequence-driven, rereacted set
of the original library Gm-cl004 which was prepared from
root cDNA. The mRNA was isolated from entire roots of 8
day old 'Williams' seedlings which were propagated on
paper towels with distilled water. Stratagene's cDNA
Synthesis kit (catalog #200431) was used to synthesize
the cDNA. The Gm-cl004 library was constructed by Dr.
Paul Keim & Virginia H. Corryell, Department of Biology,
Box 5640, Northern Arizona University, Flagstaff, AZ 86011
email: paul.keim@naui.edu, virginia.corryell@naui.edu. The
contig analysis to select unique genes was performed by
the laboratory of Ernest Retzel, Computational Biology
Centers, University of Minnesota,
http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html
Rearranging was performed by Genome Systems, St. Louis,
http://www.genomesystems.com, and sequencing by the Keck
Center for Comparative and Functional Genomics,
University of Illinois,
http://www.life.uiuc.edu/biotech/keck.html."

FEATURES source

RESULT 8
745989
EXONS
DEFINITION
745989 377 bp mRNA EST 04-AUG-1998
9252 Lambda-PRL2 Arabidopsis thaliana cDNA clone 136M317, mRNA
sequence.
ACCESSION 745989
VERSION 745989.1 GI:2762692
KEYWORDS EST.
SOURCE
thale cress.
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsids.
REFERENCE
1 (bases 1 to 377)
Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh
J., Ohlroge, T., Raikhel, N., Somerville, S., Thomas, M., Retzel
E. and Somerville, C.
Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
Plant Physiol. 106, 1241-1255 (1994)
95148729
On Jan 9, 1998 this sequence version replaced gi:934237.
Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
Lansing, MI
Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@bm.ci.msu.edu
Seq primer: T7 dye primer.
Location/Qualifiers
1. 377
/organism="Arabidopsis thaliana"
/strain="var columbia"
/db_xref="taxon:3702"
/clone_lib="136M317"
/clone_lib="Lambda-PRL2"
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
siliques). The vector is BR's lambda Zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using

FEATURES source

Query Match 30.7%; Score 331.8; DB 21; Length 803;
Best Local Similarity 73.8%; Pred. No. 2.9e-82;
Matches 405; Conservative 0; Mismatches 144; Indels 0; Gaps 0;
428 atttgaaggaaggaattctcttgtaagcgaatgaagatataattcaaatatttca 467
|||||
800 ATCTCAGAGGAAATGAGTCTNNITGTGAGGTGGATGATGATATNNATCAGATGNNTTIN 741
|||||
488 acctttgaggaaggaaggaattctcttgtaagcgaatgaagatataattcaaatatttca 547
|||||
740 NNNATGTGGGTGANNAGTCAGTSCCTCTACTATGANNATGCCCTTCAATNNANNNG 681
|||||
548 atgttgagctctccacagatgagatttactgaglyaaagacgacatgaattggaatcag 607
|||||
680 AGCTCGAGTGTGCGATGTCACATGTCACGAGGAGAACAGAAATGATGATGATGATGATG 621
|||||
608 ctctgagagatgctatagct 557
|||||
620 CGCGGGAATGCTTTATGCTCTGATTCATGCGAGATATGCTGTGACCAAGGAATGG 551
|||||

```

/db_xref="taxon:3702"
/clone="1320227"
/clone_lib="Lambda-PR12"
/note="Vector: lambda zip-Lox; Site_1: Sal; Site_2: Not;
Lambda PR12 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day roots; 2) etiolated seedlings; 3) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark-rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
siliques). The vector is BRL's lambda zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
oligo dt primed cDNA."

BASE COUNT      95 a      59 c      85 g      133 t      14 others
ORIGIN

Query Match      29.8%; Score 321.4; DB 39; Length 386;
Best Local Similarity 94.4%; Pred. No. 1.9e-79;
Matches 337; Conservative 0; Mismatches 18; Indels 2; Gaps 1;

QY 308 cctttcctccacatctactaaactcagcttctcgtatggtggaactcgaaactgagtg 367
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1  CCITTTCCCTTCACATCTACTTAAACTCAGCTTCTGTAIGTGGAATCGGAACACTGATAGTN 60

QY 368 aagggtctaatgtgagtgagtcggagggtgatgatacgtcgtggaatctcttggtttga 427
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 AAGGTCGTGTCGTCAGTGGATCGGAGGCGTGAATGATGATACGTCGTGGATCTCTTGGTTTGA 120

QY 428 atttgaaggggaatgatttcttctgtaagtcgaggaattatattcaagatgatttca 487
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 121 ATTGAGAGGGGAATNATTTCTCTGTAAGTCGATGAAGATTATATTACGATGATTCA 180

QY 488 atcttctgtgttaagtggtgcaagtccttactatgattgacacttgatctcatttag 547
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 181 AICTTTGTGGTTAAGTGGTCAAGTCCCTTACTATGATTATNCACITTNANCTATTNAG 240

QY 548 atgttgatgttccacacagtgagatgtttactgatacagcagcatgaaatggtgaaacag 607
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 241 ATGTTGATGCTTCCACAGTCAGATGTTTACINATGAACAGCATCAAAATGTCGAATCAG 300

QY 608 ctgctgagatgctatagttc--tattcaatgcttgcatttgactactaaagg 662
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 301 CTGCTGAGTGTATATATGGGCTTATTTCATGTTTCGTNNCAATTGACTNCTTNAAG 357

FEATURES             10
AW277268
LOCUS
DEFINITION
S:590403.y1 GM1019 Glycine max cDNA clone GENOME SYSTEMS CLONE 19;
G:019-2405 5' similar to SW:KC2C_ARATH P40229 CASEIN KINASE II
BETA' CHAIN ;, mRNA sequence.
ACCESSION
AW277268
VERSION
AW277268.1 GI:6665809
KEYWORDS
EST.
SOURCE
soybean.
ORGANISM
Glycine max
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; euroids 1;
Fabales; Fabaceae; Papilionoideae; Glycine.
REFERENCE
AUTHORS
Shoemaker,R., Keim,P., Vodkin,L., Erpeldein,J., Corvill,V., Khanna
A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
,R., Ritter,E., Kohn,S., Shin,I., Jackson,Y., Cardenas,M., McCann
,R., Waterston,R. and Willson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501 St. Louis, MO 63108, USA

Query Match      30.4%; Score 328.6; DB 39; Length 377;
Best Local Similarity 92.3%; Pred. No. 1.9e-81;
Matches 348; Conservative 0; Mismatches 28; Indels 1; Gaps 1;

120 ttttggagaggaatcgaattatgtacaaaggaactagtgga-ggagtggtggtggtggt 178
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1  TTTTGGAGAGGAGTATGAAATTATGTCACAGGAACGTAGNNGNAGAGAGGTGTTGGTGGGI 60

179 catcgatcagagatcctcgtgtgagctatcgtatcgaggaacgaaatcaacgatacactca 238
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 CATCCAGATCAGATCCTCGTGAGCTATGATCGGAACGATCGAATCAACGATCACTCA 120

239 ataagaactagaagaatcttccacttccacccacacatctagaggttlltcttctctaaag 298
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 ATAGAAGCTAGAGAAATCTCAACTTCCACCCACACATCTAGGGTTTNTCTTCTIAAG 180

299 acaagatcctcttcttccatctactaaactcagcttctcgtatggtggaactcgaaa 358
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 ACAAGATCCCTTTCTCTTACATCTACTTAAACTCAGCTTCTGATGATGATGATGATGAT 240

359 ctgacatcgaagatctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 418
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
241 CTGATAGTNAAGGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300

419 agtttgaatttgaaggggaatgattcttctcgtgagatcagatgatacctcgtgagatctct 478
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
301 GGTTTTGTAACTGAGAGGGGAATNANTTCNTTAACTGCTTGAAGGTTTNTTCAAG 360

479 atgattcgaattctgt 495
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
361 NTNGTTCACACTTCT 377

SOURCE      9
3841
T45841
DEFINITION
9104 Lambda-PR12 Arabidopsis thaliana cDNA clone 1320227, mRNA
sequence.
ACCESSION
T45841
VERSION
T45841.1 GI:2762564
KEYWORDS
EST.
SOURCE
thale cress.
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; euroids 1;
Brassicaceae; Brassicaceae; Arabidopsids.
REFERENCE
AUTHORS
Newman,T., deRuijter,F.J., Green,P., Keegstra,K., Kende,H., McIntosh
,L., Ohlroge,J., Raike,N., Somerville,S., Thomasow,M., Retzel
,E. and Somerville,C.
Public Soybean EST Project
Unpublished (1999)
Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PR1, Michigan State University, Plant Biology Bldg., E.
Lansing, MI
Tel: 517-353-0854
Fax: 517-353-9468
Email: 22313c@bim.cl.msu.edu
Seq primer: 17 dye primer.
Location/Qualifiers
1..386
/organism="Arabidopsis thaliana"
/strain="var columbia"

```



```

QY      970  Tgatact 976
      | | |
Db      481  TAAAGCT 487

RESULT  ;;
AM433059
LOCUS   655 bp      mRNA
DEFINITION
  s104a06.y1 Gm-cl029 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
  Gm-cl029-203 '5' similar to SW:K02B_ARATH P40228 CASEIN KINASE II
  HFTA CHALN .. mRNA sequence.
ACCESSION   AM433059.1 GI:6964366
VERSION     AM433059
KEYWORDS    EST.
SOURCE      soybean.
ORGANISM    Glycine max
            Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
            Magnoliophyta; eudicotyledons; core eudicots; Rosidae; euroids I;
            Fabales; Fabaceae; Papilionoideae; Glycine.
            1 (bases 1 to 655)
REFERENCE   1
AUTHORS    Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
            A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
            Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
            Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
            R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
            R., Waterston,R. and Wilson,R.
            Public Soybean EST Project
            Unpublished (1999)
            Contact: Shoemaker K/Public Soybean EST project
            Public Soybean EST project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
  
```

```

call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
Insert length: 603 Std Error: 0.00
High quality sequence stop: 449.
Location/Qualifiers
1. 655
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl029-203"
/clone_lib="Gm-cl023"
/tissue_type="very young cotyledons of greenhouse grown
plants"
/lab_host="DH10B"
/notes="Vector: pSPOR11; Site 1: Not I; Site 2: Sal I; This
cDNA library was constructed from mRNA isolated from very
young cotyledons (20-50mg fresh weight) of greenhouse
grown plants. The library was prepared using the Life
Technologies pSuperScript cDNA library construction kit.
Complementary DNA was synthesized from mRNA using a
poly(dT) sequence with a Not I restriction site. Sal I
linker adapters were ligated to the blunt-ended cDNA
fragments followed by Not I digestion. The cDNA fragments
were directionally cloned into the Not I-Sal I restriction
site of the pSPOR11 vector. The ligated cDNA fragments
were transformed into E.coli Electromax DH10B host cells.
This library was constructed by Dr. Paul Keim and Dr.
Virginia Corryell."
BASE COUNT 196 a 131 c 154 g 172 t 2 others
ORIGIN

```

Query Match 26.9%; Score 290.6; DB 22; length 655;
Best Local Similarity 74.9%; Pred. No. 9.5e-71;
Matches 362; Conservative 0; Mismatches 121; Indels 0; Gaps 0

```

332 ctcagcttctctgagtggaatcggaaactgataagtggaaggtctgagtgagtgatgag 391
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
162 CTAACACTCAATACGGGGATATTGAACAAAGATGTCGAAGTACTGATGTTAGTCTTTTCA 221
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
392 aggggtgatgatacgtctggtgagctctcttggctttgttaatttgagaggaagattctct 451
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
222 AAGGGGATGACACACTCTTGGAICTCATGCTTTGCAATTTGAGAGCAAAATGAATCTTTT 281
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
452 ggaagtcgataagaatatalatcaagatgatttcaatttttqgqtltaagtgagcaag 511
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
282 GCGAAGTTGATGATGATTTGCGGCAAGATGATTTCAAGCTCTCTGGATTAAGTASCAAG 341
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
512 tcccttaactatgallatgcaactgactctctctttagatgtttagctcttcccaacagtgaga 571
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
342 TCCCTACTATGATATATGACATGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 401
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
572 tatttactgatdaagacgatgaatgggtggaatcagctgctgagatgctatggtcttta 631
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
402 CTTACAGGAGGACCAAAATGAGTTAAATTTGAATCTGCAGACAAATGCTNTATGGTCTCA 461
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
572 tttactgatdaagacgatgaatgggtggaatcagctgctgagatgctatggtcttta 631
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
462 TTCAATGCCCGATACATTTTCACAAAGCAAAAGGAATGCTGCAATGCTTCACAAAGTAC 521
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
692 actgtgacttggggagatcccgagaggtttctgtgttgctgagctgagcttctccagtg 751
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
522 ACTACAAATTTGGCGGATGCTCAAGATNTTCTGCTCTCGACAAACCCCTCCCTCGGGTG 581
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
752 gacaatccgatcccgagatgagtaactgttgaagataactgctcctaataatcgaggata 811
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
582 GCCACTCACAIGTCTCTAGGTCAGTACTCTCAAGATATATTTGCCCCAGGCTGTGAGGACA 641
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
312 tat 8:4
    |||
642 TGF 644
    |||

```

```

ULF 12
71192 US AW777192 543 bp mRNA EST 12-MAY-2005
INITIATION Str2-A7 Sugar Beet germination cDNA library Beta vulgaris cDNA
clone #103 5' similar to Casein: kinase, beta chain, mRNA sequence.
SESSION AW777192
SION AW777192.1 GI:7728936
WORDS EST.
RCE beet.
ORGANISM Beta vulgaris
REFERENCE Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
AUTHORS Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae;
TITLE Caryophyllales; Chenopodiaceae; Beta.
JOURNAL 1 (bases 1 to 543)
COMMENT de los Reyes,B.G., McGrath,J.M., Myers,S. and Derrico,C.
Differential gene expression in sugar beet seedlings (Beta vulgaris
) germinated under stress conditions
Unpublished (2000)
Contact: J. Mitchell, McGrath
Sugar Beet Genetics Lab., USDA/ARS/Sugar Beet and Bean Research
Unit.
Michigan State University
494 Plant and Soil Sci. Bldg., East Lansing MI 48824, USA
Tel: (517)-432-2355
Fax: (517)-337-6782
Email: mitchmcg@pilot.msu.edu
Seq primer: T3
High quality sequence stop: 511.
Location/Qualifiers
1..543
/organism="Beta vulgaris"
/cultivar="USH20"
/db_xref="taxon:3555"
/clone="#103"
/clone_lib="Sugar Beet germination cDNA library"
SOURCE

```

```

/tissue_type="whole seedlings"
/dev_stage="4-day germination under stress (salt/NaCl,
dehydration/Mannitol and anaerobic stress)"
/lab_host="SOLR"
/note="Organ: seeds; Vector: pBluescript II KS (+) excised
from Lambda Uni-zap XR; Site_1: EcoRI; Site_2: XhoI; cDNAs
were derived from reverse transcription of pooled mRNA
samples from stressed seedlings (germinated for 4 days in
150mM NaCl, 200mM Mannitol, submerged in distilled water
and 0.3% hydrogen peroxide). The cDNA library was
generated by directional ligation of the cDNAs in the
EcoRI and XhoI sites of Lambda Uni-zap XR vector
(Stratagene). The library was excised as a pBluescript
plasmid from Lambda Uni-zap XR by EXAssist helper phage
and plated on SOLR host cells."
BASE COUNT 160 a 104 c 121 g 158 t
ORIGIN

```

```

Query Match 26.6%; Score 286.8; DB 24; Length 543;
Best Local Similarity 72.6%; Pred. No. 1.le-69;
Matches 405; Conservative 0; Mismatches 137; Indels 16; Gaps 2;
QY 387 atcgaggggtgatgatacgtctggtgactctctgttttgaatttgagaggaatgattt 446
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 ATCTGATGGTGAGGATACAGCATGCTTTCATGGTTTGCATTTGCCAGGGAATGAAT 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 447 cttctgtgaatcgatgaagatallatcaagatgatttcaacttldlglltaagtg 506
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 TTTCTGTGAGATTGATGATGATACATCCAGATGATTTCAATCTTTGTGATTTGAGCAG 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 507 tcaagctcctactatgattgactgactgactcatttagatgtttagcttcccaag 566
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 CCAAGTTCCATTTATGATTACGCACTCGACTCAITTTGATTTGAATCTTC----- 174
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 567 tgagatgtttactgatgaacagcatgaaatggtggaatcagctgctgagatgctatatgg 626
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 175 -----TCATGAGGAACAGATGAGTTGATTTCAATCTCGCGCAGAAATGCTTTATGG 225
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 627 tttattactgtctcttaccattttgaactactaaagagatgctgcaatgacagagaagta 686
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 226 CTTGATCTATGTTTCGATCATTTTACTAGTAAAGGAATGCTGCTATGTAAGAAAGAA 285
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 687 caagaactgtgatttcggagatgcccagagagtttctgttgcgctgacttctctccc 746
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 286 TAAAAAATGANTTTTCGGGTTGTCCAGAGATTACTGCTCTGCGCAGGC--GGCTTTCC 344
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 747 agttggacaatccgataccccgagatgagtagtactgtgagatatactgctttaaagcga 806
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 345 TGTTGGCCCATCAGACATTCACGATCAAGCACCTGAAATCTACTGCCCAAAATGTCA 404
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 807 quatatacttaccgcgacalcaaatccaaagcaaatattgatgagcglattttggaac 866
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 405 AGACATCTATCAACCAAGTCCGAATACCAAGCAATGTGGATGTGATACATAGGAC 464
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 867 cacatccctcactgttctctgactgactacaggaactaaagccgagagacotactca 926
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 465 TACATTCCTACCTTTTCTTCGTGATACGCAACCTTTTGCCCACTCAAGCAACTAA 524
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 927 aagctatgtcccaaaaat 944
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 525 AACCTATGTGCGGAGGAT 542
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 13
BE405491
LOCUS BE405491 562 bp mRNA EST 21-JUL-2000
DEFINITION WHE1216_H11_P222S Wheat etiolated seedling root cDNA library
Triticum aestivum cDNA clone WHE1216_H11_P22, mRNA sequence.
ACCESSION BE405491
VERSION BE405491.1 GI:9364959
KEYWORDS EST.
SOURCE bread wheat.

```

ORGANISM

Triticum aestivum

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Triticum.

1 (bases 1 to 562)

Anderson, C.D., Chao, S., Choi, B.W., Close, T.J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.E., and Tsou, J.C.

The structure and function of the expressed portion of the wheat genomes

Unpublished (2000)

Contact: Olin Anderson

US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA

Tel: 5105595773

Fax: 5105595818

Email: anderso@pw.usda.gov

Sequence have been trimmed to remove vector sequence and low

quality sequence with phred score less than 20

Seq primer: Strategene SK primer.

Location/Qualifiers

FEATURES

Source

1..562
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4577"
/clone="WHE1216_H11_P22"
/clone_lib="Wheat etiolated seedling root cDNA library"
/tissue_type="root"
/dev_stage="Five day old elicited seedling"
/lab_host="E. coli SGR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; Seeds were surface-sterilized
germinated and grown aseptically in the dark at room
temperature on filter paper with water, mystatin and
cefotaxime in covered crystallization dishes. Roots were
harvested. The tissue, total RNA, and poly(A) RNA were
prepared, a cDNA library was made, and the cDNA clones
were in vivo excised to give paluescript phagemids in the
TO Clone lab (Choi, Close, Fenton) at the University of
California, Riverside. Plasmid DNA preparations and DNA
sequencing were performed in the CD Anderson lab (all
other authors)."

E COUNT 148 a 118 c 143 g 153 t

JIN

Query Match 25.8%; Score 279; DH 35; Length 562;

Best Local Similarity 75.2%; Pred. No. 1.6e-67;

Matches 348; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

346 ggggaatcggaactgaagtgaaggctctatgtgagtgatcgagggatgatacag 405

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

100 GAAGAAATGGAACAGTAGTGAAGATCTGATGTTCTGAGAGGAGACACACA 159

406 tctgsgatctcttqatlttgtaattctgagggaggaacgalltctctgtaagtgaatgaa 465

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

160 TCTTGCAATTCATGGTCTGTGACGTGGCAGGCAACGAATCTCTGTGAGATCATGAT 219

466 gatttatatacagatgatttcaaatcttctgtgttaagtgtgtaagtcctactatgat 525

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

220 GATTATATACAGATGATTTTCAATCTCTGCGGCTTAAAGCAGTCAGGTGCCATTTATGAT 279

526 tatgcaactgactctattttagatgtctgatgtctcaacagtgagatgttactatgtaa 585

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

280 TATGCACATTCATCTCATCTCAGACATCGAGCTTCTTAATGTTGATCTATCTACCTACGAG 339

586 cagcatgaaatggtagaatcgaactctcagatgattatgqcttcttctcattcgtttac 645

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

340 CAATAATGAATTAATCAGCATCTCAGAGATGCTGTATGTTTAAATCATCTCAGGATC 399

646 atttgactactcaaggaatggctcaatgactgagaagtacagaactgtgatttcggg 705

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

400 ATCTTAACCCAGCAAGGGTCTAGTCGCAATGTTAGAAAAGTTCAGAACTATGATTTGGC 459

QY 706 agatgcccagagagtttctgtcgtgcgtcagctcttcttccagttgacaatccgatactc 765

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

DB 460 AGATGCCCTCTGTACTACTCTGTGTGTCACACCTGTCTTCAGCAGGCAATCAGACAT 519

QY 766 ccaagatcagagtaactggaagatatactgccctaaatgcgagg 808

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

DB 520 CCTAGGTCAAGCACAGTGAAGGTGTTTGTCCAAAATGTGAAG 562

RESULT 14

AI901529/C

LOCUS

618006F05.xl 618 - Inbred Tassel cDNA Library

27-JUL-1999

DEFINITION

sequence.

AI901529

VERSION

AI901529.1 GI:5607862

KEYWORDS

EST.

SOURCE

Zea mays.

ORGANISM

Zea mays.

REFERENCE

1 (bases 1 to 634)

AUTHORS

Walbot, V.

TITLE

Maize ESTs from various cDNA libraries sequenced at Stanford

UNIVERSITY

Unpublished (1999)

CONTACT: Walbot V

DEPARTMENT OF BIOLOGICAL SCIENCES

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

tel.: 650 723 2227

fax: 650 725 8221

email: walbot@stanford.edu

PLATE: 6.8006 row: F column: C5.

Location/Qualifiers

1..634

/organism="Zea mays"

/cultivar="Ohio43"

/db_xref="taxon:4577"

/clone_lib="618 - Inbred Tassel cDNA Library"

/tissue_type="tassel"

/dev_stage="tassel"

/lab_host="XLOLR"

/note="Organ: tassel; Vector: pAD-GAL4-2.1 (Hybrizap);

Inbred tassel library from Schmidt lab"

BASE COUNT 178 a 143 c 142 g 171 t

ORIGIN

Query Match

24.9%; Score 269.2; DB 13; Length 634;

Best Local Similarity 72.4%; Pred. No. 9.4e-65;

Matches 349; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 509 aagtcctactatgattatgcactctatctcatttttagatgttgatgcttccaaagtg 568

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

DB 634 AGGTGCCATATTAGATTATGCATCTGCATCTATCTATCTAGCATCTTCTTAAATGATG 575

QY 569 agatgttactgatgaacacagatgaaatggtgaaatcagctgctgagatgctatagtc 628

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

DB 574 ACGGTTTACCGAGGAGCAAAATGAATTAATCGAGTATCTGCGAGAGATCTGTACGGTT 515

QY 529 ttatcctgtctgttactatttgactactaaaggaatggtcgaatgactgagaagataca 688

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

DB 514 TAAATCATCCAGACATCTTAAACCCAGCAGGCTGTAGCTGCAATGTTGGGAAGTTCA 455

QY 689 agaactglatctcggaagatgcccgagagatcttctgttcggtcagctcttcttccag 748

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

DB 454 AGAACTACGACTTGTGTAGATGCCCGAGGCTGTACTCTGTGCGCCAGCCCTTCCTCCAG 395

QY 749 ttgacaatccgatatccccagatcgagtagctgtgaagatatactgcccataatgcgagg 808

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

DB 394 CAGGCAATCAGATGTTCTTAGATCGAGCATCTGTGAAGATATATTGTCCGAATGGGAG 335

.....

Hit No.	Query			DB	ID	Description
	Score	Match	Length			
1	1080	100.0	1060	21	258536	Arabidopsis circad
2	182	16.9	968	20	241367	Human normal uter
3	180.4	16.7	6873	21	250910	Recombinant human
4	180.4	16.7	8430	21	250911	Recombinant human
5	104.6	9.7	335	18	X83406	Breast cancer tumor
6	104.6	9.7	335	19	V69018	DNA molecule encod
7	36.4	3.4	1648	13	Q25532	Sequence of genom
8	35.8	3.3	5181	16	Q80911	Plasmodium falcipa
9	35.6	3.3	3308	21	A26917	Essential Staphylo
10	35.2	3.3	2841	16	V74488	Staphylococcus aur
11	35.2	3.3	5558	16	V52236	Streptococcus pneu
12	35	3.2	22960	20	X13282	Enterococcus faeca

PT New CKB3 gene and protein sequences used to alter circadian rhythms and

flowering in plants

Claim 1: Fig 2; 51pp; English.

The present sequence is that of *Arabidopsis thaliana* cDNA encoding CKB3 (see Y59955), a protein that interacts specifically with CCA1 and which is a structural and functional homologue of the regulatory (beta) subunit of protein kinase CK2 in *Arabidopsis*s. The cDNA was identified through use of the yeast two-hybrid system using CCA1 as bait. Recombinant plants that overexpress CKB3 have been constructed. Overexpression of CKB3 results in increased CK2 activity and results in shorter periods of rhythmic expression of CCA1 and LHY, as well as of 4 other circadian clock-controlled genes. This leads to a significant shortening of time to flowering under short-day conditions, but no phenotypic changes in morphology. Alteration of CK2 activity, particularly through the overexpression of the CKB, represents a new and effective way of modulating flowering time in plants.

Sequence 1080 BP; 299 A; 216 C; 247 G; 324 T; 0 other;

```

every Match      100.0%; Score 1080; DS 21; Length 1080;
PreSt Local Similarity 100.0%; Pred. No. 0;
atches 1080; Conservative 0; Mismatches 0; Indels 0;

```

[illegible]

Cy	721	tctctgtgagtcagtcagtccttctccagtttgagacaatccgatatcccgagatcagtgact	780
Db	721	tctcgttcgagtcagtccttctccagtttgagacaatccgatatcccgagatcagtgact	780
Oy	781	gtgaagatatactccctaaatgcgagagatatcttaccgcgatatcccaattccaagc	840
Db	781	gtgaagatatactccctaaatgcgagagatatcttaccgcgatatcccaattccaagc	840
Oy	841	aattattgagcggtactcttgggaacacattccctcacttctgtcttctgattgacttcagg	900
Db	841	aattattgagcggtactcttgggaacacattccctcacttctgtcttctgattgacttcagg	900
Oy	901	aacttaagccgcgagaagcctactcaaaagctatgtcccaaaaattcttgggtccaagta	960
Db	901	aacttaagccgcgagaagcctactcaaaagctatgtcccaaaaattcttgggtccaagta	960
Oy	961	cacaaacattgatatactagtcctctgcattctcaatctgggtgatacatttagtggctctgtaa	1020
Db	961	cacaaacattgatatactagtcctctgcattctcaatctgggtgatacatttagtggctctgtaa	1020
Oy	1021	ttgcatccggalgaagcaactgaacagatagctggcgtagctggagagatcacatcaaccatt	1080
Db	1021	ttgcatccggalgaagcaactgaacagatagctggcgtagctggagagatcacatcaaccatt	1080
RESULT	2		
ID	241367	standard; cDNA: 968 BP.	
XX	241367;		
XX	241367;		
DT	19-JAN-2000	(first entry)	
DE	Human normal uterus tissue derived cDNA 43.		
KW	Human; uterus; cancer; treatment; anticancer; cytostatic; gene therapy;		
KW	EST; expressed sequence tag; ss.		
XX	Homo sapiens.		
XX	DN19817946-A1.		
XX	21-OCT-1999.		
XX	17-APR-1998; 98DE-1017946.		
XX	17-APR-1998; 98DE-1017946.		
PA	(META-) METAGEN GFS GENOMFORSCHUNG MBH.		
PI	Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;		
XX	WPI; 1999-591956/51.		
XX	New nucleic acid sequences expressed in normal uterine tissues, and		
PT	derived polypeptides, for treatment of uterine cancer and		
PT	identification of therapeutic agents -		
XX	Claim 3; Page 106; 154pp; German.		
XX	This invention describes novel cDNA sequences (A) highly expressed in		
CC	normal uterine tissue which can have anticancer and cytostatic activity		
CC	and can be used for gene therapy. (A) are used (i) for recombinant		
CC	expression of polypeptides (B) and (ii) to isolate complete genes.		
CC	(B) are used (i) to identify agents suitable for treatment of uterine		
CC	cancer; (ii) directly for treating this form of cancer (including		
CC	expression from gene therapy vectors) and (iii) for generation of		
CC	specific antibodies. (A) are identified by assembling ESTs (expressed		
CC	sequence tags) from a particular tissue type before comparison of		
CC	expression patterns. This allows a significantly longer fragment of the		
CC	gene to be revealed, so should reduce the number of failures associated		
CC	with the fact that ESTs from different libraries may represent		

different parts of the same unknown gene, distorting the estimated frequency of occurrence in a particular tissue. 241325-741385 represent the human uterine tissue derived cDNA fragments of the invention which encode the protein fragments represented in Y59638-Y59692.

Sequence 958 A; 241 A; 286 C; 218 G; 223 T; 0 other;

```

Very Match      15.9%; Score 182; Db 20; Length 968;
1st Local Similarity 56.5%; Pred. No. 8.3e-46;
Matches 338; Conservative 0; Mismatches 260; Indels 0; Gaps 0;

```

[illegible]

	Location/Qualifiers
Key	

Query Match 16.7%; Score 180.4; DB 21; Length 6873;
Best Local Similarity 57.4%; Pred. No. 6.8e-45;

complement (1494..1530)
 /*tag= a
 /label= ori
 2014..2031
 /*tag= b
 /label= T7_promoter
 2094..2738
 /*tag= c
 /product= "Human beta-Casein"
 2803..2850
 /*tag= d
 /label= T7_terminator
 2900..3547
 /*tag= e
 /product= "Casein kinase II beta subunit"
 3571..4746
 /*tag= f
 /product= "Casein kinase II alpha subunit"
 4823..4870
 /*tag= g
 /label= T7_terminator
 complement (5897..5963)
 /*tag= h
 /label= Ptac_promoter
 /note= "Comprises multiple cloning site and
 transcriptional terminator rrrB7112"
 complement (5984..6868)
 /*tag= i
 /product= "L. delbrueckii Iminopeptidase"
 6053..6868
 /*tag= j
 /product= "Kanamycin resistance marker"
 /phenotype= "Kanamycin resistance"

WO2000098174-A1.
 17-FEB-2000.
 06-AUG-1999; 99WO-US17873.
 07-AUG-1998; 98US-0131028.
 (ABBO) ABBOIT LAB.
 Mukerji P, Lemmel SA, Leonard AE, Chaudhary S;
 WPI: 2000-205721/18.
 P-PSDB: Y70004, Y70003, Y70004, Y70005, Y70006.
 Recombinant construct useful for producing human milk protein, edible
 plant protein, antibody, antigen or hormone, comprises nucleotide
 sequences expressing beta-casein protein -
 Disclosure: Fig 7: 73pp: English.
 The patent discloses a method of producing human milk protein, edible
 plant protein, antibody or an antigen in a host cell. It involves
 transforming host cells with a vector comprising the gene
 of interest linked to a promoter and nucleotide sequences encoding
 subunits of a kinase, resistance marker and a peptidase. This method is
 useful for improving the genetic stability of a plasmid-containing
 cell during fermentation. Proteins produced may be used in
 pharmaceutical or nutritional compositions and in vaccine formulations.
 The present sequence is the plasmid construct pRAB-84-69, encoding
 recombinant human beta-casein. It comprises genes encoding human
 beta-casein, casein kinase II alpha and beta subunits, bacterial
 kanamycin resistance marker and iminopeptidase.
 Sequence 6873 BP; 1729 A; 1762 C; 1749 G; 1633 T; 0 other:

[illegible]

04-MAY-1999 (first entry)

Mouse pheromone receptor VR2 coding sequence.

Pheromone receptor; signal transduction; fertility; behaviour;
reproduction; rodent; insect; mouse; ss.

Mus sp.

W09900422-A1.

07-JAN-1999.

30-JUN-1998; 98WO-US13680.

30-JUN-1997; 97US-0051284.

(HARD) HARVARD COLLEGE.

Buck L, Dulac C, Herrada G, Matsunami H;

WPI: 1999-095684/08.

P-PSDB; W94912.

New isolated pheromone receptor polypeptides - used to develop
products for controlling fertility and behaviour in vertebrates and
invertebrates

Claim 23; Page 178; 308pp; English.

The invention relates to polynucleotide sequences encoding mammalian
pheromone receptor polypeptides. The polypeptides are expressed in
murine and rat vomeronasal organ. The products can be used for modifying
pheromone activity, e.g. for decreasing pheromone receptor mediated
signal transduction. They can be used for controlling fertility and
behaviour in vertebrates and invertebrates. Compositions comprising the
polypeptides are particularly useful in e.g. controlling fertility in
livestock and controlling reproduction in rodents or insects by
interrupting the normal behaviours of rodents or insects that result in
reproduction. The present sequence represents the coding sequence of
mouse pheromone receptor VR2.

Sequence 2424 BP: 682 A; 487 C; 504 G; 751 T; 0 other;

Query Match 3.2%; Score 34.8; DB 20; Length 2424;
Best Local Similarity 52.0%; Pred. No. 1.4;
Matches 78; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

433 agagggaatgattctctgtggaagtgcgattatattcaagatgattcaattt 492

130 agggagtgtctatttacccttggaaaactaatgaaccattggaatagatttataat 189

433 tctgatttaagtggtcaagtccttactatataattatgaactgacttcatttagatgtt 552

130 tatgatttaagtctttagaattgcagggaagtgaatatagactctctctgttaattgtttt 249

553 gatgcttccaacagtggaatttactgat 582

250 gctactgatgagatcaacaagaatccttat 279

Job 15

372

X05812 standard; cDNA; 2821 BP.

X05812:

04-MAY-1999 (first entry)

Mouse pheromone receptor VR12 encoding cDNA.

Pheromone receptor; signal transduction; fertility; behaviour;
reproduction; rodent; insect; mouse; ss.

Mus sp.

Key Location/Qualifiers

CDS 60..995

/*tag= a

W09900422-A1.

07-JAN-1999.

30-JUN-1998; 98WO-US13680.

30-JUN-1997; 97US-0051284.

(HARD) HARVARD COLLEGE.

Buck L, Dulac C, Herrada G, Matsunami H;

WPI: 1999-095684/08.

P-PSDB; W94912.

New isolated pheromone receptor polypeptides - used to develop
products for controlling fertility and behaviour in vertebrates and
invertebrates

Claim 15; Page 106-108; 308pp; English.

The invention relates to polynucleotide sequences encoding mammalian
pheromone receptor polypeptides. The polypeptides are expressed in
murine and rat vomeronasal organ. The products can be used for modifying
pheromone activity, e.g. for decreasing pheromone receptor mediated
signal transduction. They can be used for controlling fertility and
behaviour in vertebrates and invertebrates. Compositions comprising the
polypeptides are particularly useful in e.g. controlling fertility in
livestock and controlling reproduction in rodents or insects by
interrupting the normal behaviours of rodents or insects that result in
reproduction. The present sequence represents a cDNA encoding a mouse
pheromone receptor VR12. The cDNA is deposited under the Genbank
accession number AF011422.

Sequence 2621 BP: 809 A; 568 C; 561 G; 883 T; 0 other;

Query Match 3.2%; Score 34.8; DB 20; Length 2821;
Best Local Similarity 52.0%; Pred. No. 1.5;
Matches 78; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

433 agagggaatgattctctgtggaagtgcgattatattcaagatgatttcaattt 492

189 agggagtgtctatttacccttggaaaactgatgaacctattggaatagatttataat 248

493 tctgatttaagtggtcaagtccttactatgattgacttgacttgacttcatttagatgtt 552

249 tatgatttaagtctttagaattgcagggaagtgaatatagactctctctgttaattgtttt 308

553 gatgcttccaacagtggaatttactgat 582

309 gctactgatgagatcaacaagaatccttat 338

Search completed: November 15, 2000, 12:58:26

Job time: 5482 sec

